

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 15, 2003, 03:42:07 ; Search time 233 Seconds

(without alignments)  
2577.268 Million cell updates/sec

Title: US-09-600-932-2

Perfect score: 1484

Sequence: 1 NNGFASLRNRQFLLVFL.....NDTECHLTMFVCEFIKKK 277

Scoring table:  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_plus\_p2n.model -DEV=exp  
-O=/cgn2\_1/USP10-SP001/US09600932/runat\_09062003\_094530\_25971/app\_query.fasta\_1.455  
-DB=N.Geneseq\_101002 -OFMT=fastp -SUFFIX=ring -MINMATCH=0.1 -IOFCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum2 -TRANS=align40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pro -NOR=ext -HEADSIZE=500 -MUTLEN=0 -MUTLEN=2000000000  
-USER=US09600932 -ACGN\_1.1.208 -tunat\_09062003\_094530\_25971 -MCP=6 -ICPD=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMECUT=120 -WARN\_TIMECUT=30 -THRAD=5 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N.Geneseq\_101002:\*

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22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1484	100.0	1595	20	AAx88323	Human collectin cd
2	1472	99.2	1016	20	AAz33973	Human PRO702 nucle
3	1472	99.2	1016	21	AAz78480	Human PRO702 (UNO3
4	1472	99.2	1016	22	AAz45974	Human DNA encoding
5	728	49.1	813	24	ABa91207	Human collectin po
6	728	49.1	813	24	ABa91176	Human collectin po
7	719.5	48.5	1238	21	AAz58385	Human collectin en
8	719.5	48.5	1238	21	AAz58385	Human collectin en
9	719.5	48.5	1238	22	AAz465084	Membrane-bound pro
10	719.5	48.5	1238	22	AAz465084	Human PRO1182 (UNQ
11	719.5	48.5	1238	24	ABz95644	Human angiotensin
12	719.5	48.5	1238	24	ABz95644	Human PRO1182 cDNA
13	719.5	48.5	1238	21	AAz94946	Human carboxylate
14	716.5	48.3	1341	24	ABa91171	Human collectin en
15	696.5	46.9	990	22	AAz98390	Human collectin en
16	696.5	46.9	1008	22	AAz51559	Human EST-derived
17	693	46.7	1139	24	ABa91172	Human polynucleoti
18	686	46.2	735	24	ABa91202	Human collectin en
19	652.5	44.0	1269	24	ABa91199	Collectin PCR prim
20	649.5	43.8	741	24	ABa91209	Human collectin po
21	646.5	43.6	1269	24	ABa91200	Collectin PCR prim
22	643.5	43.4	741	24	ABa91210	Human collectin en
23	626	42.2	1067	24	ABa91174	Human collectin en
24	623.5	42.0	936	22	AAz51560	Human polynucleoti
25	621.5	41.9	663	24	ABa91205	Human collectin po
26	620	41.8	1067	24	ABa91175	Human collectin en
27	613	41.3	663	24	ABa91206	Human collectin po
28	577	38.9	1197	24	ABa91198	Human collectin po
29	562	37.9	669	24	ABa91208	Human collectin po
30	554	37.3	591	24	ABa91204	Human collectin po
31	554	37.3	995	24	ABa91173	Human collectin en
32	502	33.8	477	24	AAz91203	Human collectin po
33	405	27.3	707	22	AAz91268	Human digestive sy
34	366	24.1	232	21	AAz43156	Human secreted exp
35	357.5	24.1	1373	23	ABz93208	DNA encoding novel
36	337	22.7	1410	24	ABz64622	Human CDNA differe
37	337	22.7	1410	24	ABz64622	Lung cancer relate
38	328.5	22.1	1392	19	AAz4080	mu-NEO-r DNA fragm
39	328.5	22.1	1534	16	AAz92554	Bovine conglutinin
40	327.5	22.1	774	24	ABz14790	DNA encoding chick
41	283.5	19.8	1010	21	AAz70738	Pig serum lectin p
42	289.5	19.5	684	20	AAz9295	Mannan-binding pro
43	289.5	19.5	747	20	AAz07142	Human mannan-bindi
44	289.5	19.5	900	24	ABz14771	DNA encoding human
45	289.5	19.5	3605	20	AAz07143	Human mannan-bindi

## ALIGNMENTS

RESULT 1  
AAx88323  
AAx88323 standard; cDNA; 1595 BP.

AC AAX88323;  
XX 30-SEP-1999 (first entry)  
DT Human collectin cDNA.

XX Homo sapiens.  
OS Collectin; human; antibacterial; antiviral; treatment; infection; ds.  
XX Homo sapiens.

XX Key Location/Qualifiers  
FH 6..839  
FT CDS /\*tag- a  
FT /product- "collectin"

XX WO933767-A1.  
 XX 29-JUL-1999.  
 XX 24-JUL-1998; 98WO-JP033328.  
 XX 23-JAN-1998; 98JP-0011281.  
 XX (FUSO ) FUSO PHARM IND LTD.  
 XX Wakamiya N.  
 XX WPI: 1999-458691/38.  
 XX P-PSDB; AAY25518.  
 XX New collectin protein of human origin and DNA encoding it  
 XX Claim 2: Page 39-42; 58pp; Japanese.  
 XX This invention describes the isolation and characterization of a novel  
 XX human collectin protein and its encoding polynucleotide. The human  
 XX collectin exhibits antibacterial and antiviral activity and can be used  
 XX as an agent for the treatment of human bacterial and viral infections.  
 XX This sequence encodes the novel human collectin.  
 XX  
 SQ Sequence 1595 BP; 444 A; 322 C; 382 G; 447 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 6,63e-133 Length: 1595  
 Score: 1484.00 Matches: 277  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-600-932-2 (1-277) x AAX8323 (1-1595)  
 QY 1 MetAsnGlyPheAlaSerLeuLeuArgAsnGlnPheIleLeuLeuValLeuPheLeu 20  
 DB 6 ATGATGGCTTGGCTTCCTTCCTCGAAGAAACCAATTATCCCTCGTCTGCTATTTCTT 65  
 QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40  
 DB 66 TTGCAAAATTCAGAGCTGCTGCTGATATGATAGCCGCTCTACCGCTGAAGTCTGCGC 125  
 QY 41 ThrHisThrIleSerProGlyProGlyAspAspGlyGlyGlyGlyGlyGlyGlyGly 60  
 DB 126 ACACACACATTTCCACGACGCCAAGAGAGATGATGTAAGAAAGAGATCCAGAGAA 185  
 QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProGlyGlyIleLysGlyGlyLeuGly 80  
 DB 186 GAGGGAAAGATGCGCAAGTGGAGCGATGGGCCGCAAGAAATTAAGAGAACTGGGT 245  
 QY 81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysGlyAspLys 100  
 DB 246 GATATGGAGATCGGGGCAATATTTGGCAAGCTGGGCCCATTTGGAGAAAGGTGACAAA 305  
 QY 101 GlyGlyLysGlyLeuLeuGlyIleProGlyLysGlyGlyLysAlaGlyThrValCysAsp 120  
 DB 306 GGGGAAAAAGGTTTCTTGGATACCTTGGAATAAAGCAAGCAAGAGTACTGTGTGAT 365  
 QY 121 CysGlyArgGlyArgLysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140  
 DB 366 TGTGGAAATACCGGAAATTTGTTGGACACTGGATATATATATGCCCCGCTCAACACA 425  
 QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlyLysThrGluGlyLysPheThr 160  
 DB 426 TCTATGAAGTTTGTCAAAATGTGATACAGAGATGAGAAATGAAAGAAATTTCTAC 485  
 QY 161 TyrIleValGlnGluGlyLysAsnTyrArgGlnSerLeuThrHisCysArgIleArgGly 180  
 DB 486 TACATCGTCAGAGAGAGAAAGAACTACAGGAATCCCTAACCACCTCAGAGATTCGGGGT 545

QY 181 GlyMetLeuAlaMetProLysAspGluAlaIleAsnThrLeuIleAlaAspThrValAla 200  
 DB 546 GGAATCTAGCCCTAGTCCCAAGATGAGTGCACACACTGCTGACTATGTGCTC 605  
 QY 201 LysSerGlyPhePheArgValPheIleGlyLysAsnAspLeuGluArgGlyGlnTyr 220  
 DB 606 AAGAGTGGCTTCTTGGGCTGTTGATTCGCGTAATGACCTTGAAGAGGAGGACAGTAC 665  
 QY 221 MetPheThrAspAspThrProLeuGlnAsnTyrSerAspThrAspGluGlyLysProSer 240  
 DB 666 ATGTTACAGACACACCTCCACTGCAAGACTATAGCACTGGAATGAGGGGACCCACAC 725  
 QY 241 AspProGlyGlyHisGlnAspCysValGluMetLeuSerSerGlyArgThrAspThr 260  
 DB 726 GACCCCTATGCTATGAGAGCTGTGAGAGATGCTGAGCTGCGCAGATGAGATGACACA 785  
 QY 261 GluCysHisLeuThrMetTyrPheValCysGluPheIleLysLysLys 277  
 DB 786 GAGTGCATCTTACATGATGTTGTTGATGATGATGATGATGATGATGATGATGATGAT 836  
 RESULT 2  
 AA233973  
 ID AA233973 standard; cDNA; 1016 BP.  
 AC AA233973;  
 DT 07-DEC-1999 (first entry)  
 DE Human PRO702 nucleotide sequence.  
 DE Human PRO702 nucleotide sequence.  
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridization;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein; ss.  
 OS Homo sapiens.  
 XX  
 XX PN WO9446281-A2.  
 PD 16-SEP-1999.  
 XX  
 XX 08-MAR-1999; 99WO-US05028.  
 XX 10-MAR-1998; 98US-0077450.  
 XX 11-MAR-1998; 98US-0077632.  
 XX 11-MAR-1998; 98US-0077641.  
 XX 12-MAR-1998; 98US-0077649.  
 XX 12-MAR-1998; 98US-0077791.  
 XX 13-MAR-1998; 98US-0078004.  
 XX 17-MAR-1998; 98US-0040220.  
 XX 20-MAR-1998; 98US-0078886.  
 XX 20-MAR-1998; 98US-0078910.  
 XX 20-MAR-1998; 98US-0078936.  
 XX 20-MAR-1998; 98US-0078939.  
 XX 25-MAR-1998; 98US-0079294.  
 XX 26-MAR-1998; 98US-0079636.  
 XX 27-MAR-1998; 98US-0079663.  
 XX 27-MAR-1998; 98US-0079664.  
 XX 27-MAR-1998; 98US-0079689.  
 XX 27-MAR-1998; 98US-0079728.  
 XX 27-MAR-1998; 98US-0079786.  
 XX 30-MAR-1998; 98US-0079920.  
 XX 30-MAR-1998; 98US-0079923.  
 XX 31-MAR-1998; 98US-0080105.  
 XX 31-MAR-1998; 98US-0080107.  
 XX 31-MAR-1998; 98US-0080165.  
 XX 31-MAR-1998; 98US-0080327.  
 XX 01-APR-1998; 98US-0080328.  
 XX 01-APR-1998; 98US-0080333.  
 XX 01-APR-1998; 98US-0080334.  
 XX 08-APR-1998; 98US-0081049.  
 XX 08-APR-1998; 98US-0081070.

PR 08-APR-1998; 98US-0081071.  
 PR 09-APR-1998; 98US-0081195.  
 PR 09-APR-1998; 98US-0081203.  
 PR 09-APR-1998; 98US-0081229.  
 PR 15-APR-1998; 98US-0081817.  
 PR 15-APR-1998; 98US-0081838.  
 PR 15-APR-1998; 98US-0081952.  
 PR 15-APR-1998; 98US-0081955.  
 PR 21-APR-1998; 98US-0082568.  
 PR 21-APR-1998; 98US-0082569.  
 PR 22-APR-1998; 98US-0082700.  
 PR 22-APR-1998; 98US-0082704.  
 PR 22-APR-1998; 98US-0082804.  
 PR 23-APR-1998; 98US-0082767.  
 PR 23-APR-1998; 98US-0082796.  
 PR 27-APR-1998; 98US-0083336.  
 PR 28-APR-1998; 98US-0083332.  
 PR 29-APR-1998; 98US-0083352.  
 PR 29-APR-1998; 98US-0083495.  
 PR 29-APR-1998; 98US-0083496.  
 PR 29-APR-1998; 98US-0083499.  
 PR 29-APR-1998; 98US-0083500.  
 PR 29-APR-1998; 98US-0083545.  
 PR 29-APR-1998; 98US-0083554.  
 PR 29-APR-1998; 98US-0083558.  
 PR 29-APR-1998; 98US-0083559.  
 PR 30-APR-1998; 98US-0083742.  
 PR 05-MAY-1998; 98US-0084366.  
 PR 06-MAY-1998; 98US-0084414.  
 PR 06-MAY-1998; 98US-0084441.  
 PR 07-MAY-1998; 98US-0084598.  
 PR 07-MAY-1998; 98US-0084600.  
 PR 07-MAY-1998; 98US-0084627.  
 PR 07-MAY-1998; 98US-0084637.  
 PR 07-MAY-1998; 98US-0084639.  
 PR 07-MAY-1998; 98US-0084640.  
 PR 07-MAY-1998; 98US-0084643.  
 PR 13-MAY-1998; 98US-0085333.  
 PR 13-MAY-1998; 98US-0085338.  
 PR 13-MAY-1998; 98US-0085339.  
 PR 15-MAY-1998; 98US-0085573.  
 PR 15-MAY-1998; 98US-0085579.  
 PR 15-MAY-1998; 98US-0085580.  
 PR 15-MAY-1998; 98US-0085582.  
 PR 15-MAY-1998; 98US-0085589.  
 PR 15-MAY-1998; 98US-0085697.  
 PR 15-MAY-1998; 98US-0085700.  
 PR 15-MAY-1998; 98US-0085704.  
 PR 18-MAY-1998; 98US-0086022.  
 PR 22-MAY-1998; 98US-0086392.  
 PR 22-MAY-1998; 98US-0086414.  
 PR 22-MAY-1998; 98US-0086430.  
 PR 22-MAY-1998; 98US-0086486.  
 PR 28-MAY-1998; 98US-0087096.  
 PR 28-MAY-1998; 98US-0087106.  
 PR 28-MAY-1998; 98US-0087208.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 11-SEP-1998; 98US-0100038.

XX (GETH ) GENENTECH INC.

XX Wood Wt, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI; 1999-551358/46.  
 XX P-PSDB; AAY41698.

PT New secreted and transmembrane polypeptides and their polynucleotides,  
 PT useful for treating blood coagulation disorders, cancers and cellular  
 PT adhesion disorders.

PS Claim 2; Fig 36; 530P; English.

XX The present invention describes secreted and transmembrane polypeptides

CC and their polynucleotides. The nucleotide sequences are useful as  
 CC sources of probes, primers, for chromosome mapping, and for generation  
 CC of antisense sequences. They can also be used to create transgenic  
 CC animals. The proteins can be used to treat a variety of diseases and  
 CC disorders, depending on their function. Diseases that may be treated  
 CC include blood coagulation disorders, cancers and cellular adhesion  
 CC disorders. They may also be used to raise antibodies. AA23391 to  
 CC AA23338, and AAY41685 to AAY41774 represent polynucleotide and  
 CC polypeptide sequence given in the exemplification of the present  
 CC invention.

XX SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Mismatches:	Indels:	Gaps:
Score: 1472.00	1016	275	1	0	0
Percent Similarity: 99.648					
Best Local Similarity: 99.288					
Query Match: 20					

US-09-600-932-2 (1-277) x AA233973 (1-1016)

QY 1 MetanGlyPheAlaSerLeuValArgAsnGlnPheIleLeuValLeuPheLeu 20  
 DB 22 ATGAATGGCTTTCATCTTGCCTGAGAAACCAATTATTCCTCTGTAATTCCT 81  
 QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspArgProThrAlaGlnValGlyAla 40  
 DB 82 TTCGAATTCAGAGTCTGGGCTGATATGATGATGATGATGATGATGATGATGATGAT 141  
 QY 41 ThrHisThrIleSerProGlyProGlyGlyAspAspGlyGlyGlyGlyGlyGlyGly 60  
 DB 142 ACACACACAAATTCACACAGACCCAAAGAGATGATGATGATGATGATGATGATGATGAT 201  
 QY 61 GluGlyLeuHisGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 80  
 DB 202 GAGGGAAGACATGCGCAATGGGAGCGATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 261  
 QY 81 AspMetGlyAspArgGlyValAsnIleGlyValThrGlyProIleGlyValGlyGlyAsp 100  
 DB 262 GATATGGAGATCAGGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 321  
 QY 101 GlyGlyLeuGlyLeuLeuGlyValLeuProGlyGlyValGlyValGlyValGlyValGly 120  
 DB 322 GGGGAAAGAGGTTTGGTGGAAATCCTGGGAAAGAGGAAAGAGGAAAGAGGAAAGAGGAA 381  
 QY 121 CysGlyArgGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 140  
 DB 382 TGTGGAAGATACCGGAATTTGTTGACAACTGATATGATATGATATGATATGATATGATAT 441  
 QY 141 SerMetLeuPheValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 160  
 DB 442 TCTATGAAGTTTGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 501  
 QY 161 TyrIleValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180  
 DB 502 TACATGTCGAGGAAAGAGAAAGAACTACAGGATCCCTAACCCACGCGAGATGGGGGT 561  
 QY 181 GlyMetLeuAlaMetProGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 200  
 DB 562 GGAATGCTAGCCATGGCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 621  
 QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlnGlnGlnGlnGlnGln 220  
 DB 622 AAGAGTGGCTTCTTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681  
 QY 221 MetPheThrAspAsnThrProLeuGlnAsnThrSerAsnThrAsnGlnGlnGlnGlnGln 240  
 DB 682 ATGTCACAGACACACACTCCACTGCAAGACTATGCACTGCAAGACTGCAAGACTGCAAG 741  
 QY 241 AspProTyrGlyHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 260

DB 742 GACCCCTATGCTGATGAGACTGTGTGAGAGATGCTGAGCTCTGACATGATGACACA 801  
 QY 261 GlucyShsIeuThMetYrPheValCysGluPheIleuYsLysLys 277  
 DB 802 GAGTGCATCTTACCATGTACTTGTCTGTGAGTTCATCAAGAAAGAAAG 852

RESULT 3  
 AAC78480  
 ID AAC78480 standard; cDNA: 1016 BP.  
 XX AAC78480;  
 AC AAC78480;  
 DT 08-FEB-2001 (first entry)  
 DE Human PRO702 (UNQ366) nucleotide sequence SEQ ID NO:96.  
 XX  
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;  
 XX expressed sequence tag; detection; cancer; ss.  
 OS Homo sapiens.  
 XX W0200053756-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-US04341.  
 XX  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 19-MAR-1999; 99US-0126773.  
 PR 21-APR-1999; 99US-0130232.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.

(GENE ) GENENTECH INC.  
 PA  
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gertlisen ME;  
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Kijavlin ID, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
 PI Shelton DL, Stewart RA, Tumas D, Williams PM, Wood WI;  
 XX WPI: 2000-611443/58.  
 DR P-PSDB: AAB44254.  
 XX  
 PT Novel PRO polypeptides and polynucleotides used in detection methods,  
 PT to target bioactive molecules to specific cells, and to modulate  
 PT cellular activities -  
 XX  
 PS Claim 2; Fig 36; 636pp; English.  
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 CC sequence tag) sequences which encode secreted or transmembrane PRO  
 CC polypeptides. The PRO polynucleotides and polypeptides have cytosolic  
 CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in

CC the isolation of the PRO polynucleotide sequences.  
 XX  
 SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 5,39e-132 Length: 1016  
 Score: 1472.00 Matches: 275  
 Percent Similarity: 99.64% Conservative: 1  
 Best Local Similarity: 99.28% Mismatches: 1  
 Query Match: 99.19% Indels: 0  
 DB: 21 Gaps: 0

US-09-600-932-2 (1-277) x AAC78480 (1-1016)

QY 1 MetAsnGlyPheAlaSerLeuLeuTrpArgAsnGlnPheIleLeuValLeuPheLeu 20  
 DB 22 ATGATGGCTTTCATCTCTGCTTGAAGAAACCAATTATCTCTGCTATTTCTT 81  
 QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40  
 DB 82 TTGCAAAATTCAGAGCTGTGGTCTGTGATATGATACCCCTACCGCTGAAGTCTGTGCC 141  
 QY 41 ThrHisThrIleSerProGlyProGlyAspAspGlyGlyGlyGlyAspProGlyGly 60  
 DB 142 ACACACACATTTTCCACGAGACCCAAAGCAGATGATGTGTAAGAAAGAGATCCAGAGAA 201  
 QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProGlyGlyLysGlyLysGlyLys 80  
 DB 202 GAGGGAAGCATGCGAAAGTGCGAGCATGGGCGCGAAGGATTAAGAGAACTGGCT 261  
 QY 81 AspMetGlyAspArgGlyAsnIleGlyLysTrpGlyProIleGlyLysGlyLysAspLys 100  
 DB 262 GATATGGAGATCAGGCGCAATTTGCGACAGCTGGCCCATTTGGAAAGAGGTGACAA 321  
 QY 101 GlyGlyLysGlyLeuLeuGlyLysLeuProGlyGlyLysGlyLysAlaGlyThrValCysAsp 120  
 DB 322 GGGGAAAAAGGTTCTCTGGAATACCTCGAGAAAGCAAGCAGTACTGTCTGTAT 381  
 QY 121 CysGlyArgGlyArgLysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140  
 DB 382 TGTGAGATACCGGAAATTTGTTGGACACTGGGATATGATTTGCTGGCTCAGACA 441  
 QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlyThrGluLysPheThr 160  
 DB 442 TCTATGAAGTTTGTCAAGATGTGATAGAGAGATAGGAAACTGAGAGAAATTTAC 501  
 QY 161 TyrIleValGlnGlnGlyLysAsnTrpArgGlyLysSerLeuThrHisCysArgIleArgGly 180  
 DB 502 TACATCGTGCAGGAAGAGAACTACAGGGGATCCCTAACCCACTGCAGGATTCGGGGT 561  
 QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200  
 DB 562 GGAATGCTAGCCATGCCCAAGATGAGAGTGCACACACATCATCATGCTGATGATGCC 621  
 QY 201 LysSerGlyPhePheArgValAlaPheIleGlyValAsnAspLeuGluArgGlyLysTrp 220  
 DB 622 AAGAGTGGCTTTCTGGGTGTTCACTGGCGGATGACCTTGAAGAGGAGGAGAGTAC 681  
 QY 221 MetPheThrAspAsnThrProLeuGlnAsnTrpSerAsnTrpAsnGlyGlyLysProSer 240  
 DB 682 ATGTCCACAGACACACACTCATCTGCAGAACTATACCACTGGAAGAGAGGAGGCCACG 741  
 QY 241 AspProTyrGlyHisGluAspCysValGluMetLeuSerSerGlyArgTrpAsnAspThr 260  
 DB 742 GACCCCTATGAGCAGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAG 801  
 QY 261 GlucyShsIeuThMetYrPheValCysGluPheIleuYsLysLys 277  
 DB 802 GAGTGCATCTTACCATGTACTTGTCTGTGAGTTCATCAAGAAAGAAAG 852

RESULT 4  
 AAS45974  
 ID AAS45974 standard; cDNA: 1016 BP.

XX AC AAS45974;  
 XX DT 18-DEC-2001 (first entry)  
 XX DE Human DNA encoding PRO polypeptide sequence #50.  
 XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;  
 KW PCR primer.  
 XX OS Homo sapiens.  
 XX PN WO20016848-A2.  
 XX PD 20-SEP-2001.  
 XX PF 28-FEB-2001; 2001WO-US06520.  
 XX PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 03-MAR-2000; 2000US-187202P.  
 PR 06-MAR-2000; 2000US-186668P.  
 PR 14-MAR-2000; 2000US-189320P.  
 PR 14-MAR-2000; 2000US-189328P.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000US-190828P.  
 PR 21-MAR-2000; 2000US-191007P.  
 PR 21-MAR-2000; 2000US-191048P.  
 PR 21-MAR-2000; 2000US-191314P.  
 PR 28-MAR-2000; 2000US-192555P.  
 PR 29-MAR-2000; 2000US-193032P.  
 PR 29-MAR-2000; 2000US-193053P.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 04-APR-2000; 2000US-194449P.  
 PR 04-APR-2000; 2000US-194479P.  
 PR 11-APR-2000; 2000US-195975P.  
 PR 11-APR-2000; 2000US-196000P.  
 PR 11-APR-2000; 2000US-196187P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 18-APR-2000; 2000US-198121P.  
 PR 18-APR-2000; 2000US-198585P.  
 PR 25-APR-2000; 2000US-198939P.  
 PR 25-APR-2000; 2000US-199550P.  
 PR 25-APR-2000; 2000US-199554P.  
 PR 03-MAY-2000; 2000US-201516P.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 05-JUN-2000; 2000US-209632P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 XX PA (GENE) GENENTECH INC.  
 XX PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski FJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX DR MPI: 2001-602746/68.  
 XX DR P-PSDB; A029073.  
 XX PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds -

PS Claim 2; Fig 99; 774pp; English.  
 XX CC Sequences AAS45925-AAS46321 represent DNA molecules encoding and PCR  
 CC primers for PRO polypeptides of the invention. The sequences of the  
 CC invention can be used to detect the presence of a tumour in a mammal by  
 CC comparing the level of expression of a PRO polypeptide in a test sample  
 CC of cells from the animal and a control sample of normal cells, whereby a  
 CC higher level of expression in the test sample indicates the presence of a  
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
 CC blood, when contacted with it. A specific polypeptide can be used to  
 CC stimulate the proliferation or differentiation of chondrocyte cells. The  
 CC PRO proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.  
 XX SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 5 39e-132 Length: 1016  
 Score: 1472.00 Matches: 275  
 Percent Similarity: 99.64% Conservative: 1  
 Best Local Similarity: 99.28% Mismatches: 1  
 Query Match: 99.19% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-600-932-2 (1-277) x AAS45974 (1-1016)  
 QY 1 MetAsnGlyPheAlaSerLeuAlaGArgAsnGlnPheIleLeuValLeuPheLeu 20  
 DB 22 ATGAAATGGCTTTCATCCCTTCCTCGAAGAAACAAATTATCTCTCGTACTATTCTT 81  
 QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrIleGluValCysAla 40  
 DB 82 TTGCAATTTACAGCTCGGCTCGATATTGATAGCCGCTCTCCCTGAAAGCTGTGCC 141  
 QY 41 ThrHisThrIleSerProGlyProGlyAspAspGlyGluGlyAspProGlyGlu 60  
 DB 142 ACACACACAAATTTCCACGAGACCACCAAGAGAGATGGTGAAGAAAGAGATCCGAGAGA 201  
 QY 61 GlnGlyLysHisGlyLysValGlyArgMetGlyProGlyGlyIleLysGlyGluGly 80  
 DB 202 GAGGAGAGAGATGCAAGTGGAGCGATGGGCCGCAAGAAATTTAAGAGAGACTGGGT 261  
 QY 81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysLysGlyAspLys 100  
 DB 262 GATATGGAGATCAGGCGCAATATTGGCAAGACTGGGCCCATTTGGAAGAGGTTGACAAA 321  
 QY 101 GlyGlnLysGlyLeuGlyIleProGlyGluLysGlyLysAlaGlyThrValCysAsp 120  
 DB 322 GGGGAAAAGAGTTTGGTGAATTCCTGGGAAAAGGCAACAGAGTCTGTGTGAT 381  
 QY 121 CysGlyArgTyrArgLysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140  
 DB 382 TGTGGAAAGATACCGGAATTTGTTGGCAACTGATATTAGTATGCTGCTGCTCAAGACA 441  
 QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGluGluLysPheTyr 160  
 DB 442 TCTATGAAGATTGTCAAGATGTGAATGAGCGGATTAAGGAACCTAAGGAATTTCTGC 501  
 QY 161 TyrIleValGlnGluGlyLysAsnTyrArgGlySerLeuThrHisCysArgIleArgGly 180  
 DB 502 TACATCGTCGAGGAAGAGAACTACAGGATCCCTTAACCCACGCGAGATTCGGGG 561  
 QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200  
 DB 562 GGAATGTACCACTGCGCAAGATGAAGCTGCCAACAACATCTCCTGCTGCTATGTTGCC 621  
 QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluGluGlyGlnTyr 220

DB 622 AAGAGTGGCTTCTTCCGGGTGTCATGCGCTGAATGACCTTGAAGGAGGACAGACATAC 681  
 QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTrpAsnGluGlnProSer 240  
 DB 662 ATGTCACAGACACACACCTCCAGACTATGACACTGAAATGAGGGGAAACCCAGC 741  
 QY 241 AspProTyrGlyHisGlnAspCysValGlnMetLeuSerSerGlyArgTrpAsnAspThr 260  
 DB 742 GACCCCTATGCTCATGAGAGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAAATGACACA 801  
 QY 261 GlnCysHisLeuThrMetTyrPheValCysGlnPheIleIleLysLysLys 277  
 DB 802 GAGTCCACATCTTACCATGTACTGTGTGTGAGTTCATCAGAGAAAAAG 852

## RESULT 5

ABAB1207  
 ID ABA91207 standard; DNA: 813 BP.

AC ABA91207;

DT 19-FEB-2002 (first entry)

DE Human collectin polynucleotide SEQ ID NO 58.

XX Human; collectin: CL-L2-1; CL-L2-2; mouse; antibacterial; virucide;

KW protein therapy; infection; ds.

XX Homo sapiens.

XX WO200181401-A1.

XX PD 01-NOV-2001.

XX PF 23-APR-2001; 2001WO-JP03468.

XX PR 21-APR-2000; 2000JP-0120358.

XX PA (FUSO) FUSO PHARM IND LTD.

XX PI Wakamiya N, Keshi H, Ohtani K, Sakamoto T, Kishi Y;

XX DR WPI; 2002-055345/07.

XX PT New collectin family proteins, designated CL-L2-1 and CL-L2-2,

XX PT expressed in kidney and for treatment and prevention of bacterial and

XX PT viral infections

XX PS Claim 20; Page 126-127; 134pp; Japanese.

XX CC The invention relates to human collectin family proteins (CL-L2-1 and

XX CC CL-L2-2, sequences given in the specification, AB556407-AB556411 and

XX CC AB556414-AB556416), their derivatives and fragments and a related

XX CC collectin (CL-L2) of mouse origin (AB556412) and polynucleotides encoding

XX CC all or part of the proteins. The proteins have antibacterial and virucide

XX CC activity and are used for protein therapy and treatment, prevention and

XX CC diagnosis of bacterial and viral infections. The present sequence is that

XX CC of a collectin polynucleotide of the invention.

XX SQ Sequence 813 BP; 211 A; 198 C; 252 G; 152 T; 0 other;

## Alignment Scores:

Pred. No.: 1e-60 Length: 813  
 Score: 728.00 Matches: 128  
 Percent Similarity: 72.11% Conservative: 53  
 Best Local Similarity: 51.00% Mismatches: 64  
 Query Match: 49.06% Indels: 7  
 DB: 24 Gaps: 2

US-09-600-932-2 (1-277) x ABA91207 (1-813)

QY 28 LeuAspIleAspSerArgProThrAlaGluValCysAlaTrpHisThrIleSerProGly 47  
 DB 65 CTGATGTCCTCAGCAGACACACA-GAGGAGCGCTGCTCTGTGAGATTCCTTGTCCCGCG 123

QY 48 ProLysGlyAspAspGlyGluLysGlyAspProGlyGluGluGlyHisGlyVal 67  
 DB 124 CTCAAAAGGGATCAGAGAGAAAAGGAGAC-----AAAGGAGCCCGAGCGCCA 174  
 QY 68 GlyArgMetGlyProLysGlyIleLysGlyGluLeuGlyAspMetGlyAspArgGlyAsn 87  
 DB 175 GGAAGAGTGGCCCTCAGAGAGAAAAGGAGACATGGGGGACAAAAGACAGAAAGGCACT 234  
 QY 88 Ile-----GlyThrGlyProIleGlyLysGlyAspLysGlyGluLysGly 104  
 DB 235 GTGGCCCGCCCATGGAATAATGGTCCCATGGCGCAAAAGTGCAAAAGACATCTGTGT 294  
 QY 105 LeuLeuGlyIleProGlyGluLysGlyLysAlaGlyThrValCysAspCysGlyArgTyr 124  
 DB 295 GATATCGGAGCCCTCGCCCGCCCATGAGAGAACCTGATTCATGTGAGTCAGTCAGTGC 354  
 QY 125 ArgLysPheValGlyLeuAspIleSerIleAlaArgLeuLysThrSerMetLysPhe 144  
 DB 355 AGGAGGCTATTGAGGAGATGACCAACAGGTCCTCACTGACCAACTGAGCTAAATTC 414  
 QY 145 ValLysAsnValIleAlaGlyIleArgGlyThrGluGluLysPheTyrTrpIleValGln 164  
 DB 415 ATAAAAAATGCTGTCTGTCGCCGCGAGACTGAGAGCAAGATCTACCTGCTGTGAAG 474  
 QY 165 GlnGluLysAsnTyrArgLysLeuThrHisCysArgIleArgGlyLysMetLeuAla 184  
 DB 475 GAGAGAGAGCGGTACACAGATGCCAGCTGTCTGCAAGCCCGAGCGGCACACTGAGC 534  
 QY 185 MetProLysAspGluIleAlaAsnThrLeuIleAlaAspTyrValAlaLysSerGlyPhe 204  
 DB 535 ATGCCCAAGACAGAGCAGCCCAATGGCTGTGATGCTTCACTGCGACAGGCTGGCCG 594  
 QY 205 PheArgValPheIleGlyValAsnAspLeuArgGluGlyGlnTyrMetPheThrAsp 224  
 DB 595 GCCGAGTCTTCATCGTATCATGACCTGAGAGAAAGGTGCTTCTGTAACCTGGAGC 654  
 QY 225 AsnThrProLeuGlnAsnTyrSerAsnTrpAsnGluGluProSerAspProTyrGly 244  
 DB 655 CGCTCCCGCATGAGACCTTCAACAGATGGCGCAGTGGAGAGCCCAACAGCGCTGTAT 714  
 QY 245 HisGluAspCysValGlnMetLeuSerSerGlyArgTrpAsnAspThrGluLysHisLeu 264  
 DB 715 GAGAGAGACTGTGTGAGAGATGGTGGCTGAGGCTGAGATGATGTGCGTCCGACAT 774  
 QY 265 ThrMetTyrPheValCysGluPheIleLysLys 275  
 DB 775 ACCATGACTTCATGTGCGAGTTGACAAAGAG 807

## RESULT 6

ABAB1176  
 ID ABA91176 standard; cDNA; 1522 BP.

XX ABA91176;

XX DT 19-FEB-2002 (first entry)

XX DE Mouse collectin encoding polynucleotide SEQ ID NO 12.

XX KM Human; collectin: CL-L2-1; CL-L2-2; mouse; antibacterial; virucide;

XX KW protein therapy; infection; ss.

XX OS Mus musculus.

XX PN WO200181401-A1.

XX PD 01-NOV-2001.

XX PF 23-APR-2001; 2001WO-JP03468.

XX PR 21-APR-2000; 2000JP-0120358.

XX PA (FUSO) FUSO PHARM IND LTD.









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PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 07-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 09-JUL-1998; 98US-0091982.
PR 10-JUL-1998; 98US-0092182.
PR 20-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0092339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096997.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.

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PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 98US-0115365.
PA (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI: 2000-072883/06.
XX P-PSDB; AAY66738.
PT Membrane-bound proteins and related nucleotide sequences
XX Claim 2; Fig 251; 822pp; English.
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
XX Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 1,1e-59 Length: 1238
Score: 719.50 Matches: 130
Percent Similarity: 67.74% Conservative: 59
Best Local Similarity: 46.59% Mismatches: 81
Query Match: 21 Gaps: 3
US-09-600-932-2 (1-277) x AAZ65084 (1-1238)
QY 3 Glyphealaserleuauargarsnclpheiileuenuyalleupheleucln 22
DB 46 GGTCTCTGCTGCGCTGAGATGAGGGGAGATGAGCCCTGAGGCTTCTATATAGC 105
QY 23 IleclnserleuaglyleuasprialeasprerArpProthrala-----gluValCys 39
DB 106 CTGCGCTTCTGTCACGCTGCCATCTGCACATCTCAGCCGCTGCGATGACGCTGC 165
QY 40 AlathrhsthrilieserProglyProlysglyspasprlyglyuysglyaspProgly 59
DB 166 TCTGTGAGATCTCTGCTCCCTGAGGCTCAAGGGGATCGGAGAGAGAGAC----- 219
QY 60 GluclnuglyshslyglysValGlyArgmetcglyProlysglylylelysglyglu 79
DB 220 ---AAAGGCGCGCGGAGCGGCTGAGAGAGTGTGCGCCCAAGGAGAGAGAGAGATG 276

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Dd	475	GGGGCAAAAGGACAGAAAGGACAGTGGTGGTTCATGAGAAATAATGTGGCCATGTGGCTCT	534
Qy	97	LYSGIYASPIYSGIYGLIYLSGLIYLEULENGIYLIETROGLIYLSGLIYLSALAGIY	116
Dd	535	AAAGGTGAAGAAAGGAGATTCGGGTGACATAGGAGACCCCTGGTCTAATGAGAACACAGGC	594
Qy	117	ThrValCysASPcysGlyArgTyrArgIshPheValGlyGlnLeuAspIleSerIleAla	136
Dd	595	CTCCCATGTGATGTGACGACGACCTGGCAAGGCATCGGGGAGATGTGACAAACAGGTCTCT	654
Qy	137	ArgLeuLysThrSerMetLysPheValLysAsnValIleAlaGlyIleArgIuThrGlu	156
Dd	655	CACCTGACCGACGACGACCTCAAGTTCATCAAGATGCTGTCCTCCCGTGTGGCGCAGCGAG	714
Qy	157	GluLysPheTyrTyrIleValGlnGluLysAsnTyrArgIuSerLeuThrHisCys	176
Dd	715	AGCAGATGTACCTCTGTGTAGAGAGAGAGAGAGCGCTACCGGAGACCCCAAGCTGTCTGC	774
Qy	177	ArgIleArgGlyGlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrIleuAla	196
Dd	775	CAGGCGCGGGGGGACACCTGAGATGCGCCCAAGAGACAGGCTCCAAATGGCTGATGGC	834
Qy	197	AspTyrValAlaLysSerGlyPhePheArgAlaPheIleGlyAlaAsnSpleuGluArg	216
Dd	835	GCATACCTGGCCCAAGCCGGCGCTGGCCGTGTCTTCATGCGCATCAACGACCTGGGAGAG	894
Qy	217	GluGlyGlnTyrMetPheThrAspAsnThrProLeuAlaAsnTyrSerAsnTyrPasnGlu	236
Dd	895	GAGGGCGCCTTGTTGTACTGTGACACACATCCCCCATGGGAGACCTTCACAAAGCGCGAGC	954
Qy	237	GlyGluProSerAspProTyrGlyHisGluAspCysValGluMetLeuSerSerGlyArg	256
Dd	955	GGTGACCCCAACAAAGCTACGACGAGAGAGACTGCTGAGATGTGTGGCTCGGGCGGC	1014
Qy	257	TyrAsnAspThrGluCysHisLeuThrMetTyrPheValGlyGlnPheIleLys	275
Dd	1015	TGGAAAGACGTGGCTGCTCCACACCAACCATGTACTTCATGTGTAGTTTGCACAAAGAG	1071
RESULT 14			
ABAG1201			
ID	ABAG1201	standard; DNA; 813 BP.	
XX	ABAG1201;		
AC			
XX			
DT	19-FEB-2002	(first entry)	
XX			
DE		Human collectin polynucleotide SEQ ID NO 45.	
XX			
KW		Human; collectin; CL-I2-1; CL-I2-2; mouse; antibacterial; virucide;	
XX		protein therapy; infection; ds.	
OS	Homo sapiens.		
XX			
PN	WO200181401-A1.		
XX			
PD	01-NOV-2001.		
XX			
PF	23-APR-2001; 2001WO-IP03468.		
XX			
PR	21-APR-2000; 2000JP-0120358.		
XX			
PA	(FUSO ) FUSO PHARM IND LTD.		
XX			
PI	Wakamiya N, Keshi H, Ohtani K, Sakamoto T, Kishi Y;		
DR	WPI; 2002-055345/07.		
XX			
PT	New collectin family proteins, designated CL-I2-1 and CL-I2-2,		
XX	expressed in kidney and for treatment and prevention of bacterial and		
PT	viral infections		
XX			
PS	Claim 2; Page 121; 134pp; Japanese.		

[illegible]





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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 15, 2003, 07:32:52 ; Search time 154 Seconds  
(without alignments)  
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Delop 6.0, Delext 7.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

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Database: Published\_Applications\_NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1472	99.2	1016	9	US-09-978-189-96	Sequence 96, Appl
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ALIGNMENTS

RESULT 1  
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: Sequence 96, Application US/09978295A  
: Patent No. US20020156006A1  
: GENERAL INFORMATION:  
: APPLICANT: Ashkenazi, Avi  
: APPLICANT: Baker, Kevin P.  
: APPLICANT: Bostein, David  
: APPLICANT: Desnoyers, Luc  
: APPLICANT: Eaton, Dan  
: APPLICANT: Ferrara, Napoleon  
: APPLICANT: Filvaroff, Ellen  
: APPLICANT: Fong, Sherman  
: APPLICANT: Gao, Wei-Qiang  
: APPLICANT: Gerber, Hanspeter  
: APPLICANT: Gertlisen, Mary E.  
: APPLICANT: Goddard, Audrey  
: APPLICANT: Godowski, Paul J.  
: APPLICANT: Grimaldi, J. Christopher  
: APPLICANT: Gurney, Austin L.  
: APPLICANT: Hillan, Kenneth J.  
: APPLICANT: Kijavini, Ivar J.  
: APPLICANT: Kuo, Sophia S.  
: APPLICANT: Napier, Mary A.  
: APPLICANT: Pan, James  
: APPLICANT: Paoni, Nicholas F.  
: APPLICANT: Roy, Margaret Ann  
: APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630P1C11  
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Gaps: 0

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RESULT 2  
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Sequence 96, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Askenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
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59	PRIOR APPLICATION NUMBER: 60/081229
60	PRIOR FILING DATE: 1998-04-09
61	PRIOR APPLICATION NUMBER: 60/081955
62	PRIOR FILING DATE: 1998-04-15
63	PRIOR APPLICATION NUMBER: 60/081817
64	PRIOR FILING DATE: 1998-04-15
65	PRIOR APPLICATION NUMBER: 60/081819
66	PRIOR FILING DATE: 1998-04-15
67	PRIOR APPLICATION NUMBER: 60/081952
68	PRIOR FILING DATE: 1998-04-15
69	PRIOR APPLICATION NUMBER: 60/081838
70	PRIOR FILING DATE: 1998-04-15
71	PRIOR APPLICATION NUMBER: 60/082566

[illegible]

; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

**Alignment Scores:**

Pred. No.:	2,66e+18	1016	
Score:	1472.00	275	
Percent Similarity:	99.64	Conservative:	1
Best Local Similarity:	99.28	Mismatches:	0
Query Match:	99.19	Indels:	0
DB:	9	Gaps:	0

US-09-600-932-2 (1-277) x US-09-978-697-96 (1-1016)

[illegible]

### RESULT 3

US-09-978-192A-96

; Sequence 96, Application US/09978192A  
; Patent No. US20020177553A1

GENERAL INFORMATION:

APPLICANT: Asinkezazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paonli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
ACIDS  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 2,66e-178 Length: 1016  
Score: 1472.00 Matches: 275  
Percent Similarity: 99.648 Conservative: 1  
Best Local Similarity: 99.288 Mismatches: 1  
Query Match: 99.198 Indels: 0  
DB: 9 Gaps: 0

US-09-600-932-2 (1-277) x US-09-978-192A-96 (1-1016)

OY 1 MelAsngLYPhAlserLeuArgrAsngInPhleLeuLeuValLeuPheLeu 20  
DB 22 ATGAATGCGCTTTCATCTCTGCGAGAAACCAATTATCTCTGCTGCTACTATTCTT 81  
OY 21 LeuGInIleGInserLeuLysAspIleAspSerArgProThrAlaGluValCysAla 40  
DB 82 TTGCAATTCAGAGTCTGGTCTGTGATATTGATACCGCTACCGCTGAGTGTGTGCC 141



QY 41 ThrHisThrIleSerProGlyProLysGlyAspAspGlyGluLysGlyAspProGlyGlu 60  
|||||  
Db 142 ACACACACATTTCCACGACGACCAAGAGATGATGAGAAAGAAATCCAGAGAGA 201  
QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProLysGlyLysLysGlyLysGly 80  
|||||  
Db 202 GAGGGAAGAGATGAGCAAGTGGGACCATGGGCGCAAGGAATTAAGAGAGAACTGGGT 261  
QY 81 AspMetGlyAspArgGlyLysAsnIleGlyLysThrGlyProIleGlyLysLysGlyAspLys 100  
|||||  
Db 262 GATATGGAGATATGAGGCAATATGGCAAGACTGGGCGCATGGGAGAGAGGTGCAAA 321  
QY 101 GlyLysGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 120  
|||||  
Db 322 GGGGAAAAAGTTTGGCTGGAAATACCTGGGAAAAAGCAAGCAAGTACTGCTGTGAT 381  
QY 121 CysGlyArgGlyArgGlyArgGlyArgGlyArgGlyArgGlyArgGlyArgGlyArg 140  
|||||  
Db 382 TGTGAGAGATACCGGAAATTTGTTGAGCAACTGGAAATTAAGTATGCTGGCTCAAGACA 441  
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlyLysGlyLysGlyLysPheTyr 160  
|||||  
Db 442 TCTATGAGAGTTTGTCAAGATGATGATGAGAGGATTAAGGAAACTGAAAGAAATTCATC 501  
QY 161 TyrIleValGlnGluLysAsnTyrArgGlyLysSerLeuThrHisCysArgIleArgGly 180  
|||||  
Db 502 TACATCTGCGAGAGAGAGAACTACAGGAACTCCCTAACCCACGACGAGATTCGGGT 561  
QY 181 GlyMetLeuAlaMetProLysAspGluAlaIleAsnThrLeuIleAlaAspTyrValAla 200  
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Db 562 GGAATGCTACCCATGCCCAAGATGAACTGCCAACAACACTCTGCTGATGTGTGTC 621  
QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTyr 220  
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Db 622 AAGATGCTGCTTCTTGGGCTTCTCATTTGGGCTGAATGACCTGTAAGAGGGGAGGACGTAC 681  
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrAsnGluGlyLysProSer 240  
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Db 682 ATGCCCAACAACAACCTCCACGACGAGACTATAGCACTGAGATAGGGGAGGCCAACAC 741  
QY 241 AspProGlyLysHisGlyAspCysValGluMetLeuSerSerGlyArgTyrAsnAspTyr 260  
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Db 742 GACCCCATATGCTATGAGGACTGTGTGAGATCTAGCTCTGCGCAGATGAGATGACACA 801  
QY 261 GluGlyHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277  
|||||  
Db 802 GAGTGCATCTTACCATGTACTTGTCTGTGAGTTCATCAAGAGAAAAAG 852

## RESULT 4

US-09-999-832A-96

Publication No. US20020192706A1

## GENERAL INFORMATION:

APPLICANT: Asinkezzi, AVI  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Fetrara, Napoleon  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PLC63  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
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PRIOR APPLICATION NUMBER: 60/077632  
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PRIOR APPLICATION NUMBER: 60/077641  
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PRIOR APPLICATION NUMBER: 60/077649  
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PRIOR APPLICATION NUMBER: 60/078939  
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PRIOR APPLICATION NUMBER: 60/079923  
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PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
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PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
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PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 2,666-178 Length: 1016  
Score: 1472.00 Matches: 275  
Percent Similarity: 99.64% Conservative: 1  
Best Local Similarity: 99.28% Mismatches: 1  
Query Match: 99.19% Indels: 0  
DB: 9 Gaps: 0

US-09-600-932-2 (1-277) x US-09-999-832A-96 (1-1016)

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QY 21 LeuglnleuglnserleuaspilaspserarprothralagluValcysala 40  
DB 82 TTGCAATTCAGAGTCGTGGCTGTGATATGATAGCCGTCTACCGCTGAAGTCTGCC 141  
QY 41 ThrhstrlleserproglyprolyglyaspaspelglylulysglyaspProglylu 60  
DB 142 ACACACACAAATTTCACGACGACCCAAAGAGATGATGTGAAAAAGAGATCCAGGAGAA 201  
QY 61 GluglylulysHsHslylulysValglargmetcelyprolysglylulysglylulysgly 80  
DB 202 GAGGGAAGAGATGAGCAAGTGGGACGATGGGGCCGAAAGAAATTAAGAGAACTGGGT 261  
QY 81 AspmetglyaspargglyaspnllleglylulysThglyProllleglylulysglyaspLys 100  
DB 262 GATATGGGAGATCCAGGCAATATTGGCAAGCTGGCCCATTTGGGAAGAGGGTGACAAA 321  
QY 101 GlyglulysglylulysleuglylulysProglylulysglylulysValaglylulysasp 120  
DB 322 GGGGAAAAAGTGTGCTTGGATATCCCTGGGAAAAAGCAAGAGAGTACTGTCTGTGAT 381  
QY 121 CyselylulyslulyslulyslulysValglulysaspleserlilealargleuysThr 140  
DB 382 TGTGGAAGATATCCGGAATTTGTGTGCAACTGTGATTTGTGCTCGCTCAAGACA 441  
QY 141 SermetlulysphevalulysaspValilaleaglylulysglulphuglulyspetyr 160

Db 442 TCTATGAAGTTTGTCAAGATGTGATACAGAGATTAGGAAGTGAAGAAATTTAC 501  
QY 161 TTTTllevaGlnGluGlnLysAsnTyrGlnuSerLeuThrHisCysAlrIleArgly 180  
Db 502 TACATCGTGCAGGAGAGAAAGAACTACAGGAAATCCCAACCCACTGACGATTCGGGGT 561  
QY 181 GtmetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200  
Db 562 GGAATGCTAGCCATCCCAAGAGATGAAGCTGCCAACACACATCCGCGATATGTTGCC 621  
QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTyr 220  
Db 622 AAGATGGCTCTCTTCGGGGTGTCTATGCGGTGATGACCTTGAAAGGAGGACAGATAC 681  
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGluGlyProSer 240  
Db 682 ATGTCCACAGACACACTCCACTGCAGACTATACCACTGATGAGGGGGAACCCAGC 741  
QY 241 AspProTyrGlyHisGluAspCysValGluMetLeuSerSerGlyArgTyrPasnAspThr 260  
Db 742 GACCCCTATGCTCATGAGAGACTGTGTGAGATGCTGAGACTGCGCAGATGGAATGACACA 801  
QY 261 GluCysHisLeuThrMetTyrPheValGlyGluPheIleLysLysLys 277  
Db 802 GAGTGCATCTTACCATGACTTGTCTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 5  
US-09-978-189-96  
Sequence 96, Application US/09978189  
Publication No. US20030004102A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kilavin, Iyar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PLC7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
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PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/079786  
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PRIOR FILING DATE: 1998-03-30  
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PRIOR FILING DATE: 1998-04-01  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
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PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952

PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081838  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/082568  
 PRIOR FILING DATE: 1998-04-21  
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 PRIOR APPLICATION NUMBER: 60/083322  
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 PRIOR APPLICATION NUMBER: 60/083495  
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 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083742  
 PRIOR FILING DATE: 1998-04-30  
 PRIOR APPLICATION NUMBER: 60/084366  
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 PRIOR APPLICATION NUMBER: 60/084414  
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 PRIOR APPLICATION NUMBER: 60/084639  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084640  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084598  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084627  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084643  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/085339  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085338  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085323  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085582  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085700  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085689  
 PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
 Pred. No.: 2,66e-178 Length: 1016  
 Score: 1472.00 Matches: 275  
 Percent Similarity: 99.648 Conservative: 1  
 Best Local Similarity: 99.288 Mismatches: 0  
 Query Match: 99.198 Indels: 0  
 Gaps: 0

US-09-600-932-2 (1-277) x US-09-978-189-96 (1-1016)

QY 1 MetAsnGlyPheAlaSerLeuLeuArgAsnGlnPheIleuLeuValIleuPheLeu 20  
 |||||  
 Db 22 ATGATGCGCTTTCATCCTTCCTCGAAGAACCATTTTCTCTCTGCTACTATTCTT 81  
 |||||  
 QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40  
 |||||  
 Db 82 TTGCAATTCAGAGTCGCGCTCGATATGATAGCCGCTCAACCGCTGAAGTCGTGCT 141  
 |||||  
 QY 41 ThrHisThrIleSerProGlyProGlyAspAspGlyGluGlyAspProGlyGlu 60  
 |||||  
 Db 142 ACACACACATTTCCACCGACCCCAAGAGATGATGATGATGATGATGATGATGATGAT 201  
 |||||  
 QY 61 GluGlyLeuHisGlyLeuValGlyArgMetGlyProGlyGlyIleLeuGlyLeuGly 80  
 |||||  
 Db 202 GAGGAAAGCATGCAAGAGTGGACCATGCGCCGCAAGAAATTAAGAGAGACGGGT 261  
 |||||  
 QY 81 AspMetGlyAspArgGlyAsnIleGlyIleThrGlyProIleGlyIleThrGlyAsp 100  
 |||||  
 Db 262 GATATGGAGATCAGGCGCATATGATGATGATGATGATGATGATGATGATGATGAT 321  
 |||||  
 QY 101 GlyIleGlyLeuLeuGlyIleProGlyGlyIleGlyLeuGlyLeuGlyLeuGly 120  
 |||||  
 Db 322 GGGGAAAAGATTGCTGCTGATATGATGATGATGATGATGATGATGATGATGATGAT 381  
 |||||  
 QY 121 CysGlyArgThrArgIlePheValGlyIleLeuAspIleSerIleAlaArgLeuIle 140  
 |||||  
 Db 382 TGTGGAAGATACCGGAATTTGTGCAACTGATATGATGATGATGATGATGATGATGAT 441  
 |||||  
 QY 141 SerMetLeuPheValIleAsnValIleAlaGlyIleArgGlyIleThrGlyLeuIle 160  
 |||||  
 Db 442 TCTATGAAGTTTGTCAAGATGATGATGATGATGATGATGATGATGATGATGAT 501  
 |||||  
 QY 161 TyrIleValGlnGlyLeuIleAsnValIleArgIleLeuIleThrIleGlyLeuIle 180  
 |||||  
 Db 502 TACATGCTGCAAGAGAGAGAACTACAGGAAATCCCTAACCCACGACGAGATTCGGGT 561  
 |||||  
 QY 181 GlyMetLeuAlaMetProIleAspGlyAlaAlaIleAsnThrIleAlaAspTyrValAla 200  
 |||||  
 Db 562 GGAATGCTAGCAATGCCCAAGATGATGATGATGATGATGATGATGATGATGATGAT 621  
 |||||  
 QY 201 LysSerGlyPhePheValIleIleGlyValIleAsnAspLeuGlyLeuGlyGlnTyr 220  
 |||||  
 Db 622 AAGAGTGGCTTCTTTCGGGTGCTCATTCGCTGAAGTGAAGTGAAGTGAAGTGAAGT 681  
 |||||  
 QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTrpAsnGlyIleProSer 240  
 |||||  
 Db 682 ATGTCCACAGACAAACATCCACATGCAAGAAATATAGCACTGATGATGATGATGATGAT 741  
 |||||  
 QY 241 AspProTyrGlyIleGlyLeuAspCysValGlyMetLeuSerSerGlyArgTrpAsnAspThr 260  
 |||||  
 Db 742 GACCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 801  
 |||||  
 QY 261 GluGlyHisLeuThrMetTyrPheValCysGlyIleLeuIleLysLysLysLys 277

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DB      802 GAGTGCATCTTACCATGTACTTGTCTGTGAGTTCATCAAGAGAAAAAG 852
RESULT 6
US-10-174-590-99
; Sequence 99, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 99
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-99

Alignment Scores:
Pred. No.:      2,66e-178      Length:      1016
Score:          1472.00        Matches:      275
Percent Similarity: 99.64%    Conservative: 1
Best Local Similarity: 99.28%  Mismatches: 1
Query Match:    99.19%        Indels:      0
DB:              9            Gaps:          0

US-09-600-932-2 (1-277) x US-10-174-590-99 (1-1016)
QY      1 MetAsnGlyPheAlaSerLeuLeuArgArgAsnGlnPheIleLeuValLeuPheLeu 20
DB      22 ATGAAATGGCTTGGATCTTCTTCGAAAGAACCAATTATCCCTCGGACATCTTCTT 81
QY      21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40
DB      82 TTGCAAAATTCAGAGTCTGGGTCTGATATGATAGCCGCTACCGCTGAAGTCTGGCC 141
QY      41 ThrHisThrIleSerProGlyProGlyGlyAspAspGlyGlyGlyGlyGlyGlyGlu 60
DB      142 ACACACACAAATTCACCCGAGACCCCAAGAGAGATATGTAAGAAAGATCCAGAGAA 201
QY      61 GluGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyGluLeuGly 80
DB      202 GAGGGAAAGCATGGCAAAAGTGGAGCGATGGGCGCAAGAAATTAAGAGAACTGGGT 261
QY      81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysLysGlyAspLys 100
DB      262 GATATGGGAGATCAGGGCAATATTTGGCAAGACTGGGCCATTTGGGAAGAGGGTGACAA 321
QY      101 GlyLysGlyLysLeuLeuGlyIleProGlyGlyLysGlyLysAlaGlyThrValCysAsp 120
DB      322 GGGGAAAAAGGTTTGGCTTGGATACCTGGAGAAAAAGCAAGCAGGTACTGTGTGAT 381
QY      121 CysGlyArgGlyTrpArgLysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140
DB      382 TGTGAAATACCCGAAATTTGTTGGACACTGATATTAATATGCTCGGCTCAAGACA 441
QY      141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGlnGluLysPheThr 160
DB      442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATAGGGAAGAACTGAAGCAAAATTTCTAC 501

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QY      161 TyrTleValGlnGlnLysAsnTrpArgGluSerLeuThrHisCysArgTleArgGly 180
DB      502 TACATGTGCAGGAGAGAGAACTACAGAGATCCCTAACCCACTGCAGGATGGGGT 561
QY      181 GlyMetLeuAlaMetProLysAspGluAlaAsnThrLeuIleAlaAspTrpValAla 200
DB      562 GGAATGCTAGCCATGGCCCAAGATGAGCTGCCACACACTATCGCTACTATGTGGC 621
QY      201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTrp 220
DB      622 AAGATGGCTTTCTTGGGTGTGATTCAGCGCTGAATGACCTTGAAGGAGGAGCAGTAC 681
QY      221 MetPheThrAspAsnThrProLeuGlnAsnTrpSerAsnTrpAsnGlnGlyGluProSer 240
DB      682 ATTCACACAGACACACTCTCCTACTGCAGACTATAGCACTGGAATGAGGGAGCCACAC 741
QY      241 AspProTyrGlyHisGluAspCysValGluMetLeuSerSerGlyArgTrpAsnAspThr 260
DB      742 GACCCATAGGCATCTTACATGTACTTGTCTGTGATTCATCAAGAGAAAAAG 852
QY      261 GluCysHisLeuThrMetTrpPheValCysGluPheIleLysLysLys 277
DB      802 GAGTGCATCTTACCATGTACTTGTCTGTGATTCATCAAGAGAAAAAG 852

RESULT 7
US-10-176-758-99
; Sequence 99, Application US/10176758
; Publication No. US2003008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 99
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-99

Alignment Scores:
Pred. No.:      2,66e-178      Length:      1016
Score:          1472.00        Matches:      275
Percent Similarity: 99.64%    Conservative: 1
Best Local Similarity: 99.28%  Mismatches: 1
Query Match:    99.19%        Indels:      0
DB:              9            Gaps:          0

US-09-600-932-2 (1-277) x US-10-176-758-99 (1-1016)
QY      1 MetAsnGlyPheAlaSerLeuLeuArgArgAsnGlnPheIleLeuValLeuPheLeu 20
DB      22 ATGAAATGGCTTGGATCTTCTTCGAAAGAACCAATTATCCCTCGGACATCTTCTT 81
QY      21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40
DB      82 TTGCAAAATTCAGAGTCTGGGTCTGATATGATAGCCGCTACCGCTGAAGTCTGGCC 141
QY      41 ThrHisThrIleSerProGlyProGlyGlyAspAspGlyGlyGlyGlyGlyGlyGlu 60

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Db 142 ACACACACAAATTTACACAGACCCAAAGAGATATGTTAAAGAGATCCAGAGAA 201  
QY 61 GLUGLYSHSLYSGLYSVALGATGMEGLYPROLYSGLYILELYSGLYLUGLY 80  
Db 202 GAGGGAAGAGCTTGGCAAGATGGGACGATGGGCGGAAGAGATTTAAAGAGAACTGGGT 261  
QY 81 ASPMETGLYASPARGLYSANILEGLYLYSTHRLYPROILEGLYLYSLYASPLYS 100  
Db 262 GATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCATTGGGAAGAGGGGTGACAAA 321  
QY 101 GLYGLULYSGLYLEULEGLYILEPROGLYGLULYSGLYLSALAGLYTHRVALCYASP 120  
Db 322 GGGGGAAGAGCTTGGCAATCTGGCAATCTGGCAATCTGGCAATCTGGCAATCTGGT 381  
QY 121 CYSGLYARGLYTRARGLYSPHEVALGLYGLINLEUASPILESERILEALARGLEULYSTR 140  
Db 382 TGTGGAAGATACCGGAATTTGTGGCAACTGGATTTAGTATGTCTGGCTGCAAGACA 441  
QY 141 SERMETLYSPHEVALYASNAVAILLEALAGLYLEARGGLUTHTGLUGLYLSPHELYR 160  
Db 442 TCTATGAAGTTGTGCAGAAATGTATGACAGGATTTGGGAATCTGGAAGAAATCTTAC 501  
QY 161 TYRILEVALGLINGLYLGLULYASNTYRARGLYLUSERTLEUTHRLSCYARGLILEARGLY 180  
Db 502 TACATCGTCAGAGAAAGAGAACTACAGGAACTCCCTAACCCCTGACAGATTCGGGT 561  
QY 181 GLYMETLEUALAMETPROLYSASPGLUALAALASANTHRLLEALASPTYRVALALA 200  
Db 562 GGAATGCTAGCCATGCCCAAGAGATGAGAGCTGACACACTGATCGCTGATGTGTGCC 621  
QY 201 LYSSEGLYSPHEPHEARVALPHEILEGLYVALASNAAPLEUGLYUAGGLUGLYLGLINTYR 220  
Db 622 AAGAGTGGCTTCTTCCGGGTCTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 681  
QY 221 METPHETHRASPANTHRLPROLEUGLNASNTYRSERANTTPASNGLYLGLINTYR 240  
Db 682 ATGTCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAACCCAGC 741  
QY 241 ASPPROTYRGLYHISGLYASPCYSVALGLUMETLEUSERGLYARGTPASAPTHR 260  
Db 742 GACCCCTATGCTATGAGAGCTGTGTGAGTGTGTGAGCTGTGTGAGTGTGTGAGTGTG 801  
QY 261 GLUCYSHSLYEURHMETLYRPHVALCYSGLYLPHLEILELYSLYSLYS 277  
Db 802 GAGTGCATCTTACCATGTACTTGTCTGTGATTCATCAAGAGAAAG 852

RESULT 8  
US-10-175-737-99  
; Sequence 99, Application US/10173706  
; Publication No. US20030013153A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C50  
; CURRENT APPLICATION NUMBER: US/10/175,737  
; CURRENT FILING DATE: 2002-06-19  
; Prior Application removed - See file Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 99  
; LENGTH: 1016  
; TYPE: DNA

; ORGANISM: Homo Sapien  
US-10-175-737-99  
Alignment Scores:  
Pred. No.: 2,666-178  
Score: 1472.00  
Percent Similarity: 99.64  
Best Local Similarity: 99.28  
Query Match: 99.19  
DB: 9  
Gaps: 0  
US-09-600-932-2 (1-277) x US-10-175-737-99 (1-1016)  
QY 1 METASNGLYPHEALASERLEUARGARGASNGINPHEILELEULEUVALPHEU 20  
Db 22 ATGAATGCTTGCATCTTGCATCTTGCATCTTGCATCTTGCATCTTGCATCTTGCATCTT 81  
QY 21 LEUGLILGLSERLEUGLYLEUASPILESERANTTPASNGLYLGLINTYR 40  
Db 82 TGTGGAAGATACCGGAATTTGTGGCAACTGGATTTAGTATGTCTGGCTGCAAGACA 141  
QY 41 THRISTHRLSETPROGLYPROLYSGLYASPARGLYGLULYSGLYASPARGLY 60  
Db 142 ACACACACAAATTTACACAGACCCAAAGAGATATGTTAAAGAGATCCAGAGAA 201  
QY 61 GLUGLYSHSLYSGLYSVALGATGMEGLYPROLYSGLYILELYSGLYLUGLY 80  
Db 202 GAGGGAAGAGCTTGGCAAGATGGGACGATGGGCGGAAGAGATTTAAAGAGAACTGGGT 261  
QY 81 ASPMETGLYASPARGLYSANILEGLYLYSTHRLYPROILEGLYLYSLYASPLYS 100  
Db 262 GATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCATTGGGAAGAGGGGTGACAAA 321  
QY 101 GLYGLULYSGLYLEULEGLYILEPROGLYGLULYSGLYLSALAGLYTHRVALCYASP 120  
Db 322 GGGGGAAGAGCTTGGCAATCTGGCAATCTGGCAATCTGGCAATCTGGCAATCTGGT 381  
QY 121 CYSGLYARGLYTRARGLYSPHEVALGLYGLINLEUASPILESERILEALARGLEULYSTR 140  
Db 382 TGTGGAAGATACCGGAATTTGTGGCAACTGGATTTAGTATGTCTGGCTGCAAGACA 441  
QY 141 SERMETLYSPHEVALYASNAVAILLEALAGLYLEARGGLUTHTGLUGLYLSPHELYR 160  
Db 442 TCTATGAAGTTGTGCAGAAATGTATGACAGGATTTGGGAATCTGGAAGAAATCTTAC 501  
QY 161 TYRILEVALGLINGLYLGLULYASNTYRARGLYLUSERTLEUTHRLSCYARGLILEARGLY 180  
Db 502 TACATCGTCAGAGAAAGAGAACTACAGGAACTCCCTAACCCCTGACAGATTCGGGT 561  
QY 181 GLYMETLEUALAMETPROLYSASPGLUALAALASANTHRLLEALASPTYRVALALA 200  
Db 562 GGAATGCTAGCCATGCCCAAGAGATGAGAGCTGCCAACACTGATCGCTGATGTGTGCC 621  
QY 201 LYSSEGLYSPHEPHEARVALPHEILEGLYVALASNAAPLEUGLYUAGGLUGLYLGLINTYR 220  
Db 622 AAGAGTGGCTTCTTCCGGGTCTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 681  
QY 221 METPHETHRASPANTHRLPROLEUGLNASNTYRSERANTTPASNGLYLGLINTYR 240  
Db 682 ATGTCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAACCCAGC 741  
QY 241 ASPPROTYRGLYHISGLYASPCYSVALGLUMETLEUSERGLYARGTPASAPTHR 260  
Db 742 GACCCCTATGCTATGAGAGCTGTGTGAGTGTGTGAGCTGTGTGAGTGTGTGAGTGTG 801  
QY 261 GLUCYSHSLYEURHMETLYRPHVALCYSGLYLPHLEILELYSLYSLYS 277  
Db 802 GAGTGCATCTTACCATGTACTTGTCTGTGATTCATCAAGAGAAAG 852

RESULT 9  
US-10-173-706-99  
; Sequence 99, Application US/10173706  
; Publication No. US20030022283A1

```

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C7
CURRENT APPLICATION NUMBER: US/10/173,706
PRIORITY APPLICATION: 2002-06-17
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 99
LENGTH: 1016
TYPE: DNA
ORGANISM: Homo Sapien
US-10-173-706-99

Alignment Scores:
Pred. No.: 2,66e-178 Length: 1016
Score: 1472.00 Matches: 275
Percent Similarity: 99.64% Conservative: 1
Best Local Similarity: 99.28% Mismatches: 1
Query Match: 99.19% Indels: 0
Gaps: 0
DB: 9

US-09-600-932-2 (1-277) x US-10-173-706-99 (1-1016)
QY 1 MetasnGLYPheAlaSerLeuLeuArGArAsnInPheIleLeuValLeuPheLeu 20
DB 22 ATGATAGCGCTTGTCATCTGCTGTCGAGAACCAATTATCTCTGCTGCTGCTGCT 81
QY 21 LeuGlnIleGlnSerLeuGlnLeuAspIleAspSerArgProThrAlaGluValCysAla 40
DB 82 TTGCAGATTCAGAGTCGTGGCTGCTGATTTGATGACCCGCTACCGCTGAACTGCTGCC 141
QY 41 ThrHisThrIleSerProGlyProLysGlyAspAspGlyGluValGlyAspProGlyGlu 60
DB 142 ACGACACACAAATTCACAGAGCCCAAGAGATGATGGAGAAAGAGATCCAGAGAGA 201
QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyGluLeuGly 80
DB 202 GAGGGAAGACATGGCAAGTGGAGCGCATGGGCGGAAAGAAATTAAGAGAACTGGGT 261
QY 81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysLysGlyAspLys 100
DB 262 GATATGGAGATCAGCGCAATATGGCAAGACTGGGCCCATTTGGAGAGAGAGGTGACAAA 321
QY 101 GlyGlyLysGlyLeuLeuGlyIleProGlyGlyLysGlyLysAlaGlyThrValCysAsp 120
DB 322 GGGGAAAAAGGTTGCTTGATGATCTGAGATACCTGGAGAAAAAGCAAGCAAGTCTGTGAT 381
QY 121 CysGlyArgLysArgLysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140
DB 382 TGTGGAAGATACCGCAAAATTTGTTGGCAACAGTGAATATGATGCTGCGCTCAAGACA 441
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlyThrGlnGluLysPheArg 160
DB 442 TCTATGAAAGTTGTCAAGATGATGATGAGGATGAGGAACTGAAAGCAAAATTCATC 501
QY 161 TyrIleValGlnGluLysAsnTyrArgLysLeuThrHisCysArgGlyIleArgGly 180
DB 502 TATCATGTGCGAGAGAAAGAACTACAGGAAATCCCTAACCCAGTGCAGGATGGGGT 561
QY 181 GlyMetLeuAlaMetProLysAspGluAlaIleAsnThrLeuIleAlaAspIlyValAla 200

```

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DB 562 GGAATGCTAGCCATGCCCAAGATGAAGCTCCCAACACTCATCGTGAATGTTGCC 621
QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTyr 220
DB 622 AAGATGGCTCTTTCGGGTGCTCATGCGGTGATGACCTTGAAGGAGGAGGACAGTAC 681
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnThrPasnGlnGlyLysProSer 240
DB 682 ATGTCCACAGACACTCCACTGCACAGACTATGACACTGAGATGAGGAGGAGCCAGC 741
QY 241 AspProTyrGlyHisGluAspCysValGluMetLeuSerSerGlyArgTyrPasnAspThr 260
DB 742 GACCCCTATGCTCATGAGACTGCTGAGAGATGCTGAGTGTGAGCAAGATGAGATGACACA 801
QY 261 GluGlyHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277
DB 802 GAGTGCACTCTTACCATGTACTTGTGTGAGTTCATCAAGAGAAAG 852

RESULT 10
US-10-175-738-99
Sequence 99, Application US/10175738
Publication No. US20030022294A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C45
CURRENT APPLICATION NUMBER: US/10/175,738
PRIORITY APPLICATION: 2002-06-19
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 99
LENGTH: 1016
TYPE: DNA
ORGANISM: Homo Sapien
US-10-175-738-99

Alignment Scores:
Pred. No.: 2,66e-178 Length: 1016
Score: 1472.00 Matches: 275
Percent Similarity: 99.64% Conservative: 1
Best Local Similarity: 99.28% Mismatches: 1
Query Match: 99.19% Indels: 0
Gaps: 0
DB: 9

US-09-600-932-2 (1-277) x US-10-175-738-99 (1-1016)
QY 1 MetasnGLYPheAlaSerLeuLeuArGArAsnInPheIleLeuValLeuPheLeu 20
DB 22 ATGATAGCGCTTGTCATCTGCTGTCGAGAACCAATTATCTCTGCTGCTGCTGCTGCT 81
QY 21 LeuGlnIleGlnSerLeuGlnLeuAspIleAspSerArgProThrAlaGluValCysAla 40
DB 82 TTGCAGATTCAGAGTCGTGGCTGCTGATTTGATGACCCGCTACCGCTGAACTGCTGCC 141
QY 41 ThrHisThrIleSerProGlyProLysGlyAspAspGlyGluValGlyAspProGlyGlu 60
DB 142 ACGACACACAAATTCACAGAGCCCAAGAGATGATGGAGAAAGAGATCCAGAGAGA 201
QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyGluLeuGly 80
DB 202 GAGGGAAGACATGGCAAGTGGAGCGCATGGGCGGAAAGAAATTAAGAGAACTGGGT 261

```



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QY      81  AspmetGlyAspArgGlyAsnIleGlyThrGlyProIleGlyLysGlyAspLys 100
      262  GATATGGAGATCAGGAGCATATGGCAAGCTGGGCGCATGGCAAGAGGATGACAA 321
QY      101  GlyGluGlyLeuLeuGlyIleProGlyGluGlyLysAlaGlyThrValCysAsp 120
      322  GGGGAAAAAGTTGCTGGTAATCCTGGAGAAAAAGCAAAACAGGTACTGCTGTGAT 381
Db      121  CysGlyArgTyrArgLysPheValGlyIleLeuAspIleSerIleAlaArgLeuLysThr 140
      382  TGTGGAGATACCGGAAATTTGTGGACAACCTGATATAGTATTCCTCGGCTCAAGACA 441
QY      141  SerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGluGlyLysPheTyr 160
      442  TCTATGAGATTGTTCAGAAATGTGATAGCAGGGATAGGAAACTGAAAGAAATTTCTAC 501
Db      161  TyrIleValGlnGluGlyLysAsnTyrArgGlySerLeuThrHisCysArgIleArgGly 180
      502  TACATCGTCGAGAGAGAGAACTACAGGAAATCCCTAACCTGCAAGATCGGGGT 561
QY      181  GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200
      562  GGAATGCTACCAATGCCCAAGATGAGCTGCCCAACACACTCATCCCTGACTATGTTGCC 621
Db      201  LysSerGlyPhePheArgValPheIleGlyValAlaAsnAspLeuGluArgGluGlyIleTyr 220
      622  AAGATGGCTTTCTTGGGTGTTCATTTGGCTGTAATGACCTGTAAGAGAGGACAGTAC 681
QY      221  MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGluGlyProSer 240
      682  ATGTCACACAGAACAACTCCACTGCAAGAACTATAGCAACTGGAATGAGGGGAAACCCAC 741
Db      241  AspProTyrGlyHisGluAspCysValGluMetLeuSerSerGlyArgTyrPasnAspThr 260
      742  GACCCCATGTGATGAGAGCTGTGTGAGAGATGCTGCGCAGATGAGATGACACA 801
QY      261  GluCysHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277
      802  GAGTGCATCTTACCATGTACTTGTCTGTGAGTTCATCAAGAGAAAAAG 852

```

## RESULT 11

```

US-10-175-752-99
; Sequence 99, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT APPLICATION NUMBER: US/10/175,752
; PRIORITY FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; Seq ID NO 99
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-752-99

```

Alignment Scores:

Pred. No.:	2,666-178	Length:	1016
Score:	1472.00	Matches:	275
Percent Similarity:	99.64%	Conservative:	1

Best Local Similarity: 99.28% Mismatches: 1  
 Query Match: 99.19% Indels: 0  
 DB: 9 Gaps: 0

US-09-600-932-2 (1-277) x US-10-175-752-99 (1-1016)

```

QY      1  MetAsnGlyPheAlaSerLeuLeuArgArgAsnGlnPheIleLeuValLeuPheLeu 20
      22  ATGATGGCTTTCGATCTCTGCTCGAAGAAACCAATTAATCCCTCGTACTATTTCTT 81
Db      21  LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40
      82  TTGCATTAATTCAGAGCTGGGTCTGTGATATTAATGACCGTCTACCGCTGGAAGTGTGCC 141
QY      41  ThrHisThrIleSerProGlyProLysGlyAspAspGlyGluGlyLysGlyAspProGlyGlu 60
      142  ACACACACAAATTTTCCAGCAGACCCCAAGAGATATGATGTGAAAAAGAGATCCAGAGAA 201
Db      61  GlyGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyGluLeuGly 80
      202  GAGGAGAAAGCATGGCAAGTGGACCGCATGGGGCGGAAAGAAATTAAGAGAACTGGGT 261
QY      81  AspmetGlyAspArgGlyAsnIleGlyThrGlyProIleGlyLysGlyAspLys 100
      262  GATATGGAGATCAGGAGCATATGGCAAGCTGGGCGCATGGCAAGAGGATGACAA 321
Db      101  GlyGluGlyLeuLeuGlyIleProGlyGluGlyLysAlaGlyThrValCysAsp 120
      322  GGGGAAAAAGTTGCTGGTAATCCTGGAGAAAAAGCAAAACAGGTACTGCTGTGAT 381
QY      121  CysGlyArgTyrArgLysPheValGlyIleLeuAspIleSerIleAlaArgLeuLysThr 140
      382  TGTGGAGATACCGGAAATTTGTGGACAACCTGATATAGTATTCCTCGGCTCAAGACA 441
Db      141  SerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGluGlyLysPheTyr 160
      442  TCTATGAGATTGTTCAGAAATGTGATAGCAGGGATAGGAAACTGAAAGAAATTTCTAC 501
QY      161  TyrIleValGlnGluGlyLysAsnTyrArgGlySerLeuThrHisCysArgIleArgGly 180
      502  TACATCGTCGAGAGAGAGAACTACAGGAAATCCCTAACCTGCAAGATCGGGGT 561
Db      181  GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200
      562  GGAATGCTACCAATGCCCAAGATGAGCTGCCCAACACACTCATCCCTGACTATGTTGCC 621
QY      201  LysSerGlyPhePheArgValPheIleGlyValAlaAsnAspLeuGluArgGlyIleTyr 220
      622  AAGATGGCTTTCTTGGGTGTTCATTTGGCTGTAATGACCTGTAAGAGAGGACAGTAC 681
Db      221  MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGluGlyProSer 240
      682  ATGTCACACAGAACAACTCCACTGCAAGAACTATAGCAACTGGAATGAGGGGAAACCCAC 741
QY      241  AspProTyrGlyHisGluAspCysValGluMetLeuSerSerGlyArgTyrPasnAspThr 260
      742  GACCCCATGTGATGAGAGCTGTGTGAGAGATGCTGAGCTGTGCAAGATGAGACACA 801
QY      261  GluCysHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277
      802  GAGTGCATCTTACCATGTACTTGTCTGTGAGTTCATCAAGAGAAAAAG 852

```

## RESULT 12

```

US-10-176-482-99
; Sequence 99, Application US/10176482
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

```

APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C70  
CURRENT APPLICATION NUMBER: US/10/176,482  
CURRENT FILING DATE: 2002-06-20  
Prior Application removed - See file Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 99  
LENGTH: 1016  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-176-482-99

## Alignment Scores:

Pred. No.: 2,666-178 Length: 1016  
Score: 1472.00 Matches: 275  
Percent Similarity: 99.64% Conservative: 1  
Best Local Similarity: 99.28% Mismatches: 0  
Query Match: 99.19% Indels: 0  
Gaps: 0

US-09-600-932-2 (1-277) x US-10-176-482-99 (1-1016)

QY 1 Metasnlglypheaaserleuauargatgaspnphelleuauvalleupheleu 20  
DB 22 ATGATGGCTTGGATCCTTGGCTGGAAGAAACCAATTATTCCTGACATTTCTT 81  
QY 21 LeuGlnIleGlnSerleuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40  
DB 82 TTGCAAAATCGAGATCGGGCTGGATTTGATAGCCGCTCCCTGAGAGTCTGGCC 141  
QY 41 ThrHisThrIleSerProGlyProIleGlyAspAspGlyGluValCysAlaProGlyGlu 60  
DB 142 ACACACACAAATTTACACGACGACCAAGAGATATGCTGTAAGAAAGAGATCCAGAGAA 201  
QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyLysLeuGly 80  
DB 202 GAGGAAAAAGGTTTGGTGGAAATACCTGGAGAAAAAGCAAGAGAGTACTGCTGTGAT 381  
QY 81 AspNetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysGlyAspLys 100  
DB 262 GATATGGAGATCGAGGCAATATGCGACAGCTGGCCCATTTGGGAAGAGGAGTGAACA 321  
QY 101 GlyLysLysGlyLeuLeuGlyIleProGlyGlyLysGlyLysAlaGlyThrValCysAsp 120  
DB 322 GGGGAAAAAGGTTTGGTGGAAATACCTGGAGAAAAAGCAAGAGAGTACTGCTGTGAT 381  
QY 121 CysGlyArgLysArgLysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140  
DB 382 TGTGGAGATACCGGAAATTTGTTGGACAACTGGATTTAGTATTTGCTCGGCTCAACACA 441  
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlnThrGlnLysPheThr 160  
DB 442 TCTATGAAGTTTGCAGAAATGCTGATGACAGGATTTAGGAACTGAAGAAATTTCTAC 501  
QY 161 TyrIleValGlnGlnLysAsnTyrArgLysSerLeuThrHisCysAlaGlyIleArgGly 180  
DB 502 TACATCGTGCAGAGAGAGAAAGAACTACAGGAAATCCCTAACCCCTCAGAGATTCGGGGT 561  
QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200  
DB 562 GGAATGCTAGCCAGCCCAAGAGATGAGCTGCCAACACATCATCGTGTGATATGTTGCC 621  
QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlyGlyTyr 220  
DB 622 AAGAGTGGCTTCTTCCTGGGCTGCTCATTTGCTGATATACCTTGAAGAGGAGGACATAC 681  
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGlnGluProSer 240

DB 682 ATGTCCAGAGACAGACCTCCAGTGCAGACTATAGAACTGGAATGAGGGGAAACCCAGC 741  
QY 241 AspNetGlyHisGlnLysPheValGlnMetLeuSerSerGlyArgTyrAsnAspThr 260  
DB 742 GACCCCTATGATCAGAGAGAGCTGTGGAGAGCTGAGAGTCTGGCAGAGATACACA 801  
QY 261 GluGlyHisLeuThrMetLysPheValCysGluPheIleLysLysLys 277  
DB 802 GATGGCATCTTACCATGTACTTTGCTGTGATTCATCAAGAGAGAAAG 852

## RESULT 13

US-10-176-757-99  
Sequence 99, Application US/10176757  
Publication No. US20030022297A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C86  
CURRENT APPLICATION NUMBER: US/10/176,757  
CURRENT FILING DATE: 2002-06-20  
Prior Application removed - See file Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 99  
LENGTH: 1016  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-176-757-99

US-09-600-932-2 (1-277) x US-10-176-757-99 (1-1016)

QY 1 Metasnlglypheaaserleuauargatgaspnphelleuauvalleupheleu 20  
DB 22 ATGATGGCTTGGATCCTTGGCTGGAAGAAACCAATTATTCCTGCTGATATTTCTT 81  
QY 21 LeuGlnIleGlnSerleuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40  
DB 82 TTGCAAAATCGAGATCGGGCTGGATTTGATAGCCGCTCCCTGAGAGTCTGGCC 141  
QY 41 ThrHisThrIleSerProGlyProIleGlyAspAspGlyGluValCysAlaProGlyGlu 60  
DB 142 ACACACACAAATTTACACGACGACCAAGAGATATGCTGTAAGAAAGAGATCCAGAGAA 201  
QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyLysLeuGly 80  
DB 202 GAGGAAAAAGGTTTGGTGGAAATACCTGGAGAAAAAGCAAGAGAGTACTGCTGTGAT 261  
QY 81 AspNetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysGlyAspLys 100  
DB 262 GATATGGAGATCGAGGCAATATGCGACAGCTGGCCCATTTGGGAAGAGGAGTGAACA 321  
QY 101 GlyLysLysGlyLeuLeuGlyIleProGlyGlyLysGlyLysAlaGlyThrValCysAsp 120  
DB 322 GGGGAAAAAGGTTTGGTGGAAATACCTGGAGAAAAAGCAAGAGAGTACTGCTGTGAT 381

```

QY 121 CysGlyArgTyrArgIysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140
DB 382 TGTGGAAATACCGGAATTTGTGGACAACTGATATTTAGTATGCTGGCTCAAGACA 441
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlnThrGlnLysPheTyr 160
DB 442 TCTATGAAGTTTGCACAAATGTGATAGCAGGATAGGGAATCTGAAGAATTTCTAC 501
QY 161 TyrIleValGlnGlnGlnLysAsnTyrArgGlnSerLeuThrHisCysArgIleArgGly 180
DB 502 TACATCGTCGACGAGAGAGAACTACAGGAAATCCCTAACCCCTCAGATTCGGGGT 561
QY 181 GlyMetLeuAlaMetProLysAspGlnAlaIleAsnThrLeuIleAlaAspTyrValAla 200
DB 562 GGAATGCTAGCCATCCCAAGAGATGAACTGCCAACACACTCATCGCTGATGTTGCC 621
QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlnArgGlyGlnTyr 220
DB 622 AAGACTGGCTCTTCTGGGGTGTTCATGCGTGAATGACCTTGAAGGGAGGACAGTAC 681
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTrpAsnGlnGlyLupProSer 240
DB 682 ATGTCCACAGACAACTCCACTGACAGACTATAGCAACTGATGAGGGGAACTCCAGC 741
QY 241 AspProTyrGlyHisGlnAspCysValGlnMetLeuSerSerGlyArgTTPAsnAspThr 260
DB 742 GACCCCTATGTCATGAGAGACTGTGTGAGATGCTGAGCTGTGGCAATGGAATGACACA 801
QY 261 GlucySHisLeuThrMetTyrPheValCysGlnPheIleLysLysLys 277
DB 802 GAGTCCCATCTTACCATGTACTTGTCTGTGAGTTTCAACAGAAAGAAAAG 852

```

## RESULT 14

```

US-10-176-913-99
: Sequence 99, Application US/10176913
: Publication No. US2003002298A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Matanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P343081C66
: CURRENT APPLICATION NUMBER: US/10/176,913
: CURRENT FILING DATE: 2002-06-20
: Prior Application removed - See file Wrapper or Palm
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 99
: LENGTH: 1016
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-176-913-99

```

## Alignment Scores:

```

Pred. No.: 2,66e-178 Length: 1016
Score: 1472.00 Matches: 275
Percent Similarity: 99.64% Conservative: 1
Best Local Similarity: 99.28% Mismatches: 1
Query Match: 99.19% Indels: 0
DB: 9 Gaps: 0

```

US-09-600-932-2 (1-277) x US-10-176-913-99 (1-1016)

QY 1 MetaAnglyPheAlaSerLeuThrArgTrpAsnGlnPheIleLeuValLeuPheLeu 20.

```

DB 22 ATCAATGCGCTTGCATCCCTGCTCGAAGAAACCAATTTATCTCTGCTGATTTCTT 81
QY 21 LeuGlnIleGlnSerLeuGlnLysAspIleAspSerArgProThrAlaGlnValCysAla 40
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGATATTTGATAGCCGTCCTTACCGCTGAAATCTGTGCC 141
QY 41 ThrHisThrIleSerProGlyProLysGlyAspAspGlyLysGlyAspProGlyGly 60
DB 142 ACACACACATTTTCCACGAGACCCCAAGAGATGATGTGAAAAGAGATCCAGAGAA 201
QY 61 GlnGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyLysLeuGly 80
DB 202 GAGGGAAGACATGCGCAAGTGGGACCATGGGGCCCAAGCAATTAAGAGAACTGGGT 261
QY 81 AsnMetGlyAspArgLysAsnIleGlyLysThrGlnProIleGlyLysLysGlyAspLys 100
DB 262 GATATGGAGATCAGGCAATATTTGCAAGACTGGGCCCATTTGGGAGAGAGGTGCACAA 321
QY 101 GlyLysLysGlyLeuLeuGlyIleProGlyGlnLysGlyLysAlaGlyThrValCysAsp 120
DB 322 GGGGAAAAAGTTTGTCTGGAATACCTGGAGAAAAAGCAAGAGTACTGTCTGTAT 381
QY 121 CysGlyArgTyrArgIysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140
DB 382 TGTGGAAGATACCGGAATTTGTGGACACAGTGAATTAATATGCTGCGCTCAAGACA 441
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlnThrGlnLysPheTyr 160
DB 442 TCTATGAAGTTTGCACAAATGTGATAGCAGGATAGGGAATCGGAAGAAATTTCTAC 501
QY 161 TyrIleValGlnGlnGlnLysAsnTyrArgGlnSerLeuThrHisCysArgIleArgGly 180
DB 502 TACATGCTGACGAGAGAGAACTACAGGAAATCCCTAACCCCTCAGATTCGGGGT 561
QY 181 GlyMetLeuAlaMetProLysAspGlnAlaIleAsnThrLeuIleAlaAspTyrValAla 200
DB 562 GGAATGCTAGCCATCCCAAGAGATGAACTGCCAACACACTCATCGCTGATGTTGCC 621
QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlnArgGlyGlnTyr 220
DB 622 AAGACTGGCTCTTCTGGGGTGTTCATGCGTGAATGACCTTGAAGGGAGGACAGTAC 681
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTrpAsnGlnGlyLupProSer 240
DB 682 ATGTCCACAGACAACTCCACTGACAGACTATAGCAACTGATGAGGGGAACTCCAGC 741
QY 241 AspProTyrGlyHisGlnAspCysValGlnMetLeuSerSerGlyArgTTPAsnAspThr 260
DB 742 GACCCCTATGTCATGAGAGACTGTGTGAGATGCTGAGCTGTGGCAATGGAATGACACA 801
QY 261 GlucySHisLeuThrMetTyrPheValCysGlnPheIleLysLysLys 277
DB 802 GAGTCCCATCTTACCATGTACTTGTCTGTGAGTTTCAACAGAAAGAAAAG 852

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## RESULT 15

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US-10-180-552-99
: Sequence 99, Application US/10180552
: Publication No. US20030022300A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Matanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P343081C66

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FILE REFERENCE: P343081C153  
CURRENT APPLICATION NUMBER: US/10/180.552  
CURRENT FILING DATE: 2002-06-25  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 99  
LENGTH: 1016  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-180-552-99

Alignment Scores:  
Pred. No.: 2,666-178 Length: 1016  
Score: 1472.00 Matches: 275  
Percent Similarity: 99.64% Conservative: 1  
Best Local Similarity: 99.28% Mismatches: 1  
Query Match: 99.19% Indels: 0  
DB: Gaps: 0

US-09-600-932-2 (1-277) x US-10-180-552-99 (1-1016)

QY 1 MetAsnGlyPheAlaSerLeuLeuArgAsnGlnPheIleLeuValLeuPheLeu 20  
DB 22 ATGAATGCTTTCATCTTCTGCTGAGAGAACCAATTATCTCTGCTGCTTCTT 81  
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DB 82 TTGCAAAATTCAGAGCTGGCTGGATGATGATAGCCCTCTACCGCTGAAGTCTGTGCC 141  
QY 41 ThrHisThrIleSerProGlyProGlyAspAspGlyGluGlyAspProGlyGlu 60  
DB 142 ACACACACAAATTTCCACGAGACCCAAAGAGATGATGTTGTAAGAGATCCAGAGAA 201  
QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProGlyGlyIleLysGlyLeuGly 80  
DB 202 GAGGAGAAAGCATGCAAAAGTGGAGCGCATGGGGCCGAAAGAAATTAAGAGAACTGGCT 261  
QY 81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysLysGlyAspLys 100  
DB 262 GATATGGGAGATCAAGGCGCAATATGGCAAGCTGGGCCCATGGCAAGAGAGGAGTACAAA 321  
QY 101 GlyGluLysGlyLeuLeuGlyIleProGlyGlyLysGlyLysAlaGlyThrValCysAsp 120  
DB 322 GGGGAAAAAAGTTTCTCTGGAATACCTGAGAAAAAGCAAGCAAGTACTGTCTGTGAT 381  
QY 121 CysGlyArgGlyArgLysPheValGlyLysLeuAspIleSerIleAlaArgLeuLysThr 140  
DB 382 TGTGGAAGATACCGGAAATTTGTTGACAACTGGATATTGCTCGGCTCAGACA 441  
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlyThrGluGluLysPheThr 160  
DB 442 TCTATGAAGTTTGTCAAGATGTGTACAGAGGATTAAGGAACTGAGAGAGAAATTTCTAC 501  
QY 161 TyrIleValGlnGluLysAsnTyrArgGluSerLeuThrHisCysArgIleArgGly 180  
DB 502 TACATCGTCAGAGAGAGAGAACTACAGGAACTCCCTAACCACTGCAGATTCGGGGT 561  
QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200  
DB 562 GAAATGCTAGCCATCCCAAGGATGAGTACCAACACATCCTGCTGACTATGTGCC 621  
QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGluGlyGlnTyr 220  
DB 622 AAGATGGCTTCTTTCGGGTGTTCAATGGCGTGAATGACCTTGAAGAGGAGGAGACATAC 681  
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPheAsnGluGlyProSer 240  
DB 682 ATGTCCACAGACAACTCCACTAGCAACTATAGCAACTGAAATGAGGGGAAACCCAGC 741  
QY 241 AspProTyrGlyHisGluAspCysValGluMetLeuSerSerGlyArgTyrAsnAspThr 260  
DB 742 GACCCCTATGTCATGAGAGACTGTGTGAGATGCTGAGCTCGGCAATGATGACACA 801

QY 261 GluCysHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277  
DB 802 GAGTGCATCTTACCAATGATCTTGTGTGAGTTGATCAAGAGAAAAAG 852

Search completed: June 15, 2003, 08:45:54  
Job time: 160 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 15, 2003, 05:56:57 ; Search time 1425 Seconds

(without alignments)  
3148.175 Million cell updates/sec

Title: US-09-600-932-2

Perfect score: 1484

Sequence: 1 MNGFASLRNMQTLLVFL.....NDTECHLTMTFVCEFKKK 277

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL-frame\_plus\_p2n.model -DEV-xip  
-Q/cgn2\_1/USPTO\_spool/US09600932/runat\_09062003\_094531\_25993/app\_query.fasta.1.455  
-DB-EST -QFMT-fastap -SUFIX-1st -MINMATCH-0.1 -LOEPC-0 -LOEPC-0  
-UNITS-bits -START-1 -END-1 -MATRIX-biosum62 -TRANS-human40.cdi -LIST-45  
-DOCALLIGN-200 -THR\_SCORE-DECT -THR\_MAX-100 -THR\_MIN-0 -ALIGN-15 -MODE-LOCAL  
-OUTFMT-PTC -NORM-ext -HEADS-500 -MINLEN-0 -MAXLEN-2000000000  
-USER-US09600932.cgn2\_1.1555 -gunat\_09062003\_094531\_25993 -MCP-6 -ICPU-3  
-NO\_MAP -LARGEDETER -NEG\_SCORES-0 WAIT -DSPLOCK-100 -LONGLOG  
-DEV-TIMEOUT-120 -MARN-TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6  
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELXT-7

Database :  
EST:  
1: em\_estba:  
2: em\_esthum:  
3: em\_estlin:  
4: em\_estnu:  
5: em\_estlov:  
6: em\_estpl:  
7: em\_estro:  
8: em\_hic:  
9: gb\_est1:  
10: gb\_est2:  
11: gb\_hic:  
12: gb\_est3:  
13: gb\_est4:  
14: gb\_est5:  
15: em\_estfun:  
16: em\_estom:  
17: gb\_gss:  
18: em\_gss\_hum:  
19: em\_gss\_inv:  
20: em\_gss\_pln:  
21: em\_gss\_vrt:  
22: em\_gss\_fun:  
23: em\_gss\_mam:  
24: em\_gss\_mus:  
25: em\_gss\_other:  
26: em\_gss\_pro:  
27: em\_gss\_rtd:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1215	81.9	752	13	BM009998 603630745
2	917	52.7	955	13	BB612129
3	782	52.7	609	13	BM010788
4	777	52.4	482	12	BF078010
5	731	49.3	489	13	BI467460
6	728	49.1	1383	11	AK003121
7	699.5	47.1	1426	11	BC009951
8	673	45.4	654	13	BI067078
9	611.5	41.2	962	14	BO927000
10	596	40.2	451	10	AM355638
11	547	36.9	380	10	BB869893
12	538	36.3	893	12	BE314316
13	532	35.8	361	10	BB869996
14	532	35.8	486	13	BM426695
15	517.5	34.9	823	13	BI198782
16	514	34.6	354	10	AM435866
17	505	34.0	962	14	BO069775
18	477	32.1	788	12	BE311981
19	474	31.9	723	10	BE382845
20	462	31.1	1239	13	BM551435
21	456	30.7	1012	10	BE260904
22	454.5	30.6	640	10	BE383325
23	453.5	30.6	672	12	BF206254
24	445.5	28.9	702	12	BF311185
25	444	28.9	1094	13	BM574424
26	441	29.7	590	10	AV690347
27	429	28.9	683	10	BE382433
28	426	28.7	326	14	R29493
29	421.5	28.4	644	10	BE262656
30	417.5	28.1	715	10	BE313199
31	414.5	27.9	916	12	BF314100
32	412	27.8	916	12	BF316717
33	411.3	27.7	564	9	AI353438
34	409.5	27.6	626	12	BF316436
35	403.5	27.2	613	12	BF312666
36	401.5	27.1	654	10	BE312923
37	400.5	27.0	767	10	BE260355
38	395	26.6	728	10	BE260359
39	388.5	26.2	892	12	BF314275
40	388	26.1	602	13	BI442205
41	384.5	25.9	1000	13	BI188831
42	378	25.5	362	14	R97480
43	376.5	25.4	538	10	BE312003
44	369.5	24.9	619	13	BI199068
45	369	24.9	697	12	BF317087

ALIGNMENTS

RESULT 1  
LOCUS BM009998  
DEFINITION 603630745F1 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:5444459 5',  
ACCESSION BM009998  
VERSION BM009998.1 GI:16524352  
KEYWORDS  
SOURCE EST.  
ORGANISM human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 752)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)









# JOURNAL COMMENT

Est discovery in swine  
Unpublished (2000)  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smithemail.marc.usda.gov  
Single pass sequencing. Bases called and alt. trimmed with phred  
v0.980904.e. Vector identified by cross-match with the -minscore 18  
and -minmatch 12 options.

## FEATURES

### Source

1. 499  
/organism="Sus scrofa"  
/db\_xref="taxon:9823"  
/clone\_lib="MARC 2P10"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI;  
Library made from pooled tissue from testis, ovary,  
endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 145 a 96 c 161 g 97 t

## Alignment Scores:

Pred. No.: 6 38e-73 Length: 499  
Score: 731.00 Matches: 140  
Percent Similarity: 94.1% Conservative: 6  
Best Local Similarity: 90.32% Mismatches: 9  
Query Match: 49.26% Indels: 0  
DB: 13 Gaps: 0

US-09-600-932-2 (1-277) x B1467460 (1-499)

QY 1 Metnnglyphea1aserleu1eua1rgr1a1ng1n1bhe1leu1eua1leu1phea1e 20  
DB 34 ATGGGTGGCTTGGAGCTGGAGCCCGAAGAAACCAAGTCACTCCCTGGGGCTCTTCTT 93  
QY 21 Leug1n1leg1nser1eug1yleu1as1p1leas1p1e1r1p1ro1h1a1g1u1a1c1y1a1 40  
DB 94 TTGCAGATTCAGAGCTCGGTCTGCACATCGACAGCTGCTGCTACCCCTGAAGTCTGCC 153  
QY 41 Thr1str1r1le1ser1p1ro1g1p1ro1g1y1a1sp1a1sp1g1y1u1y1g1a1sp1p1ro1g1y1 60  
DB 154 ACACACACAATTTCACCGACGACCAAGAGAGATGATGATGAAAAGAGATACAGAGAG 213  
QY 61 Glug1ly1sh1g1y1a1g1y1a1r1g1m1e1t1p1ro1y1s1c1y1l1e1y1s1g1y1u1e1n1g1 80  
DB 214 GAGGGAAGCATGGAGAGGAGCGAGCTGGGGCCAAAGAAATTAAGGGTGAAGTGGT 273  
QY 81 Asp1e1t1g1y1a1p1a1r1g1y1a1n1l1g1y1t1h1r1g1p1ro1l1e1g1y1l1y1s1g1y1a1sp1 100  
DB 274 GATATAGAGAGACAGGAGCAACATGGGACAGCTGGGCCCATTTGGCAAGAGGTGACAAA 333  
QY 101 Gly1g1u1y1s1g1yleu1e1n1g1y1l1e1p1ro1g1y1u1y1s1g1y1a1g1y1t1h1r1a1c1y1a1sp 120  
DB 334 GGAGAAAAGGGGTTCCCTCGGATGCTCGGAGAAAAGGCGAAGAGGTACTGCTGTGCAC 393  
QY 121 Cys1g1y1a1r1g1y1a1r1g1y1a1g1y1n1e1u1a1sp1le1ser1le1a1a1r1g1leu1y1t1h1r 140  
DB 394 TGGGGAATACCGGAAGAGTGTGGACAACTGGATATCACTGTGGCTCGCTCAAGACA 453  
QY 141 Ser1e1t1y1s1p1h1e1a1l1y1a1n1a1l1e1a1g1y1l1e1a1r1g1u1t1h1r 155  
DB 454 TCGATGAAGTTGTTCAGAGATGATATACAGAGGATTCGGGAACC 498

RESULT 6  
AK003121

LOCUS AK003121 1383 bp mRNA linear HNC 19-JAN-2002  
DEFINITION Mus musculus adult male heart cDNA, RIKEN full-length enriched  
library, clone:1010001H16;homolog to COLLECTIN 34, full insert  
sequence.  
ACCESSION AK003121 GI:12833583  
VERSION AK003121.1  
KEYWORDS HNC; CAP trapper.  
SOURCE Mus musculus (strain:C57BL/6J) adult male heart cDNA to mRNA,  
clone:1010001H16.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
MEDLINE  
PUBMED  
10349636

## REFERENCE

1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
MEDLINE  
PUBMED  
11042159

## REFERENCE

3 Shibata, K., Itoh, M., Aizawa, K., Nagata, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunaka, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, S., Nishitani, T., Harada, A.,  
Tamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watabiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1751-1771 (2000)  
20530913  
MEDLINE  
PUBMED  
11076861

## REFERENCE

4 Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,  
Aizawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanka, I.,  
Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R.,  
Kadoya, K., Matsuda, H., Ashburner, M., Balasov, S., Casavant, T.,  
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,  
Kuehl, P., Lewis, S., Matsuo, Y., Nakado, I., Pesole, G.,  
Quackenbush, J., Schriml, L.M., Staudli, F., Suzuki, R., Tomita, M.,  
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,  
Baldarelli, R., Barsh, G., Blake, J., Botfield, D., Bojunga, N.,  
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bulic, C.,  
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,  
Marchionni, L., Mashima, J., Mazzarelli, J., Mombarts, P., Nordone, P.,  
Rang, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,  
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,  
Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L.,  
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S.,  
and Hayashizaki, Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
21085660  
MEDLINE  
PUBMED  
11217851

## REFERENCE

5 (bases 1 to 1383)  
Adachi, J., Aizawa, K., Akahira, S., Akinura, T., Aono, H., Arai, A.,  
Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bulic, C.,  
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanaoka, T.,  
Hara, A., Hayatsu, N., Hill, D., Hironaka, K., Hirooka, T., Hori, F.,  
Hume, D., Imotani, K., Ishii, Y., Itoh, M., Iizawa, M., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koyama, S.,  
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,  
Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,





## ORIGIN

Alignment Scores:  
 Pred. No.: 3,47e-66 Length: 654  
 Score: 673.00 Matches: 122  
 Percent Similarity: 83.72% Conservative: 22  
 Best Local Similarity: 70.93% Mismatches: 28  
 Query Match: 45.35% Indels: 0  
 Gaps: 0

US-09-600-932-2 (1-277) x B1067078 (1-654)

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 133 CTAGAGTGGCTTTCATCTCCAGTCCAGATTGTTGGTTGATGTGCAATCGACCT 192  
 35 ThrAlaGluValCysAlaThrHisThrIleSerProGlyProGlyAspAspGlyGlu 54  
 193 ACAACAGATGTCCTCTCGACACACACTATTTTACCTGACCCAAAGGGGATGATGTGAA 252  
 55 LysGlyAspProGlyGluGluGlyHisGlyLysValGlyArgMetGlyProGlyGly 74  
 253 AAAGGAGATAGAGGAGAGAGAGGCAAAAGGAAAGTTGGACCAAAAGGACCTAAAGGA 312  
 75 IleGlyGlyGluLeuGlyAspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIle 94  
 313 AACAAAGGAGACTGGGGGATGTGCGTACCGAGGAAATGCTGGGAAATCGGCGCAT 372  
 95 GlyLysLysGlyAspLysGlyGluLysGlyLeuLeuGlyIleProGlyGlyLysGlyLys 114  
 373 GGAGGAAAGGTGACAAAGGAGCCAAAGGCAATACAGGGGTGTGCAAAAAAGGAAAA 432  
 115 AlaGlyThrValCysAspCysGlyArgTyrArgLysPheValGlyLeuAspIleSer 134  
 433 GCAGGACAGAGCTGTGACTGTGGAAGTACCGCAGAGATTGTGGCAACATGAAATATCAAT 492  
 135 IleAlaArgLeuLysThrSerMetLysPheValLysAsnValIleAlaGlyIleArgGlu 154  
 493 GTGCTCGGCTTAAACACATCCATCAAGTTGTAAAGATGTATAGCAGGCAATCAGGAG 552  
 155 ThrGluGlyLysPheTyrTyrIleValGlnGluGlyLysAsnTyrArgLysLeuThr 174  
 553 ACGGATGAAAAATCTCTATATATGTCAAAAGAGAGCAATTAACAGAGAGCCCTGATG 612  
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 613 CATTCGNNNNNCAAGNNNNNCACTGGCCATGCT 648

RESULT 9  
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 ACCESSION BQ927000  
 VERSION BQ927000.1 GI:22342031  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 962)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: rgs@bhs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov

## FEATURES

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 /note="Organ: brain; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
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 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: This is a NIH-MGC Library."

## BASE COUNT

203 a 275 c 323 g 157 t 4 others

## Alignment Scores:

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US-09-600-932-2 (1-277) x BQ927000 (1-962)

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 23 IleGlnSerLeuGlyLeuAspIleAspSerArgProThrAla-----GluValGys 39  
 111 CTGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 170  
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 171 TCTGTGCAATCT 224  
 60 GluGluGlyLysHisGlyLysValGlyArgMetGlyProGlyGlyIleLysGlyLysLeu 79  
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 282 GGAGCAAAAGGAG 341  
 97 LysGlyAspLysGlyLysGlyLysLeuGlyIleProGlyGlyLysGlyLysValAlaGly 116  
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 402 CTCCTCATGAG 461  
 137 ArgLeuLysThrSerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGlu 156  
 462 CAGCTACACAGCAGAGCTCAAGTTCATCAAGATGCTGCGCGGTGTGGCAGAGCGAGG 521  
 157 GluLysPheTyrTyrIleValGlnGluGlyLysAsnTyrArgLysLeuThrHisCys 176  
 522 AGCAAGATCTACTGCTGTGAG 581  
 177 ArgIleArgGlyLysLeuLeuAlaMetProLysAspGluAlaAlaAsnThrIleAla 196  
 582 CAGGCGCGGGGCGAGCGTGTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641  
 197 AspTyrValAlaLysSerGlyPhePheArgVal-PheIleGlyValAlaAspLeu--Glu 215







QY 190 AAlaAaenThrLeuileAlaAspTyrValAlaIaIysSerGlyPhePheArgValPheIle 209  
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 1 (bases 1 to 361)  
 REFERENCE Akimura,T., Aikawa,T., Carninci,P., Furuno,M., Hasegaki,T.,  
 Hayatsu,N., Hirose,K., Hirose,T., Hirose,T., Imotani,K., Ishii,  
 Y., Ito,M., Kawai,J., Kojima,Y., Kono,H., Kouda,M., Matsuyama,T.,  
 Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,  
 Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,  
 Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,  
 A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,  
 Watanabe,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.  
 2001)  
 TITLE Unpublished (2001)  
 JOURNAL Contact: Yoshinobu Hayashizaki  
 COMMENT Laboratory for genome exploration Research Group, RIKEN Genomic  
 Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsr.riken.go.jp,  
 url: http://genome.gsc.riken.go.jp/  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,  
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 prepare full-length cDNA libraries for rapid discovery of new  
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 Hayashizaki,Y.  
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 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,  
 Y. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.  
 e mouse tissues.

FEATURES  
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 Location/Qualifiers  
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 DB 128 GGAATTAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 187  
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 DB 188 GTGGAGCGCCAGGACCAAG 247  
 QY 87 AsnIleGlyLysThrGlyProIleGlyLysGlyAspLysGlyGlyGlyGlyGlyGlyGly 106  
 DB 248 AATATTGGCAAGCTGAGCCCTATTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307  
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 SOURCE chicken.  
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 1 (bases 1 to 486)  
 REFERENCE Cogburn,L.A., Morgan,R. and Burnside,J.  
 ESTs from Normalized Chicken fat cDNA library-USDA/IFAFS Animal



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DB 457 CTACCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516
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DB 517 CGGGGGGACAGCTGAGCATGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576
QY 199 lAlaLysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGluGly 219
DB 577 GCGGCAAGCGCGCGCTGCGCGCGCTGCTTCATCGGCGCATCAAGAGAGAGAGAGAGAG 636
QY 219 nTyrMetPheThr--AspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGluGlyGlu 238
DB 637 CTTGCTGTAACCTGAGACCACTCCCGCATGCGGAGACCTTCACAGAGTGGCGGAGGCTGAG 696
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DB 697 CCAACAATAGCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751
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GenCore version 5.1.6  
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Perfect score: 1484

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	208	14.0	876	US-09-535-521-4
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5	208	14.0	2851	US-09-535-521-1
6	208	14.0	2851	US-09-535-521-3
7	206.5	13.9	1560	US-09-453-702B-264
8	206.5	13.9	61663	US-09-453-702B-62
9	202.5	13.6	384	US-09-535-521-7
10	202.5	13.6	384	US-09-535-521-9
11	202.5	13.6	417	US-09-535-521-10
12	202.5	13.6	417	US-09-535-521-12

13	202.5	13.6	423	US-09-535-521-13	Sequence 13, Appl
14	202.5	13.6	423	US-09-535-521-15	Sequence 15, Appl
15	202.5	13.6	561	US-09-535-521-16	Sequence 16, Appl
16	202.5	13.6	561	US-09-535-521-18	Sequence 18, Appl
17	202.5	13.6	624	US-09-535-521-19	Sequence 19, Appl
18	202.5	13.6	624	US-09-535-521-21	Sequence 21, Appl
19	201	13.5	369	US-09-535-521-24	Sequence 24, Appl
20	201	13.5	369	US-09-535-521-26	Sequence 26, Appl
21	196	13.2	1333	US-09-237-357-51	Sequence 51, Appl
22	195.5	13.2	1212	US-09-581-435-10	Sequence 10, Appl
23	194.5	13.1	1212	US-09-581-435-11	Sequence 11, Appl
24	192.5	13.0	1212	US-09-591-435-9	Sequence 9, Appl
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28	183.5	12.4	2383	US-09-523-487-9	Sequence 9, Appl
29	183.5	12.4	2409	US-09-320-095-9	Sequence 9, Appl
30	179	12.1	1560	US-08-794-795-5	Sequence 5, Appl
31	179	12.1	1560	US-09-249-200-5	Sequence 5, Appl
32	177.5	12.0	1703	US-08-794-795-1	Sequence 1, Appl
33	177.5	12.0	1703	US-09-249-200-1	Sequence 1, Appl
34	177	11.9	1107	US-09-188-930-217	Sequence 217, Appl
35	175.5	11.8	885	US-08-365-103B-3	Sequence 3, Appl
36	175.5	11.8	3181	US-08-685-086-1	Sequence 1, Appl
37	175	11.8	3404	US-09-453-702B-94	Sequence 94, Appl
38	175	11.8	9827	US-09-453-702B-66	Sequence 66, Appl
39	175	11.8	45175	US-09-453-702B-116	Sequence 116, Appl
40	175	11.8	48908	US-09-453-702B-137	Sequence 137, Appl
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42	174.5	11.8	1005	US-08-365-103B-1	Sequence 1, Appl
43	174	11.7	4359	US-09-484-970B-4	Sequence 4, Appl
44	173	11.7	1608	US-09-029-348-19	Sequence 19, Appl
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#### ALIGNMENTS

RESULT 1  
US-09-198-603C-26  
; Sequence 26, Application US/09198603C  
; Patent No. 6537193  
; GENERAL INFORMATION:  
; APPLICANT: TULLY, Raymond E.  
; APPLICANT: CALTAGIRONE, G. Thomas  
; APPLICANT: MOYER, Shawn S.  
; TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC YEAST  
; FILE REFERENCE: A7290  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
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; TYPE: DNA  
; ORGANISM: CHICKEN  
US-09-198-603C-26

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US-09-600-932-2 (1-277) x US-09-198-603C-26 (1-714)

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NUMBER OF SEQ ID NOS: 26  
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 NAME/KEY: CDS  
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 US-09-535-521-4

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 QY 103 LYSGLYLEULYGLIILEPROGLYGLULYSGLYLYSGLYTHR-VALCYASPCYSGI 122  
 DB 255 -----GAAATCCAGAGCTGCCAGAGTGTACAGACATGAAGAAATCCAGCTGAACAGAA 311  
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 QY 265 RME-----TYRPHVALCYSGLU 271  
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# RESULT 4

US-09-535-521-6/c  
 Sequence 6, Application US/09535521  
 Patent No. 6410714  
 GENERAL INFORMATION:  
 APPLICANT: Weber, Eric R.  
 APPLICANT: McCall, Catherine A.  
 TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)  
 TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
 FILE REFERENCE: AL-5  
 CURRENT APPLICATION NUMBER: US/09/535,521  
 EARLIER FILING DATE: 2000-03-24  
 EARLIER APPLICATION NUMBER: 60/125,913  
 EARLIER FILING DATE: 1999-03-24  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 6  
 LENGTH: 876  
 TYPE: DNA  
 ORGANISM: Canis familiaris  
 US-09-535-521-6

Alignment Scores:  
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 Score: 208.00 Matches: 65  
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 Best Local Similarity: 26.21% Mismatches: 83  
 Query Match: 14.02% Indels: 65  
 Gaps: 7

US-09-600-932-2 (1-277) x US-09-535-521-6 (1-876)

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 DB 655 CTGGCAAGACACAAACGGTGCACCAAGATGCGCCA----- 623  
 QY 103 LYSGLYLEULYGLIILEPROGLYGLULYSGLYLYSGLYTHR-VALCYASPCYSGI 122  
 DB 622 -----GAAATCCAGAGCTGCCAGAGTGTGACAGACATGAAGAAATCCAGCTGAACAGAA 566  
 QY 122 YARGTYRARGLYSPHEVALIGLYLNUASPILESERILEALARGLEULYTHRSERME 142  
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 QY 142 TLSPHEVALYASNAVALLIAGLYILEARGGLU----- 155  
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 QY 155 ----- 155  
 DB 445 ACTCCAGAGAGAGTGAAGAGCTGTGATGAGTACACGTTGCAACGCGCTCGAGTG 386  
 QY 156 -----GLULYSPHELYTYRILEVALIGL 165  
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 QY 185 TPOLYASPGILUALAALASANTHRIEULIENALASPIRYVALIALYSSERGLYPHEPH 205  
 DB 265 CATCCAGAGAGAGAGAGAGTCTGCGCCAGAGTATGCCAACAAGAGAGGCG----- 211  
 QY 205 EARGVALPHEILEGLYVALASNPENGLUARGGLYGLINTYRMEPHEPHTHASPAS 225  
 DB 210 -----ACCTGATTTGGCTCCGCGAGCTGACAGAGAGGGGAGTTATCTGATGAGAGCA 155  
 QY 225 NTHPROLEUGLNASNTYRSEASANTTPASNGULYGLUPROSERASPPROTYRGLYHI 245









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US-09-535-521-9/C
; Sequence 9, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-9

Alignment Scores:
Pred. No.: 8.67e-15 Length: 384
Score: 202.50 Matches: 44
Percent Similarity: 55.56% Conservative: 21
Best Local Similarity: 37.61% Mismatches: 47
Query Match: 13.65% Indels: 5
DB: GAPS: 3

US-09-600-932-2 (1-277) x US-09-535-521-9 (1-384)
QY 156 GUGLUYSPhETyTyrIleValGInGLuLulysAsnTyRArgLuseRLeuThRHis 175
DB 354 CAGAGGAAGTGCTACTACTGCGGAGAGAGCCCAAGAAGTGATCCAGCCCGTTGGCC 295
QY 176 CysArgIleArgGlyGlyMetLeuAlaMetProLysAspGluAlaIAsnThRleu 195
DB 234 TGCAGCAAGCTGCAAGGCGGCTGCCCATCCACAGCCAGAGGAGCAAGCACTTCTG 235
QY 196 AlaAspTyRValAlaLysSerGlyPhePheArgValPheIleGlyValAlaAsnThR 215
DB 234 GCCAGATATGCCAACAAGAGGC-----ACCTGATATGCGCTCCGGACCTGGAC 184
QY 216 ArgGluGlyGlnTyRMetPheThRAspAsnThRProLeuGlnAsnTyRserAsnThR 235
DB 183 AGAGAGGGGGAGTTATCTGTGATGAGACGAGAACCCCTG---AACTATAGCAACTGCG 127
QY 236 GUGLUYluproSerAspProTyRgLyHsGluAspCysValGluMetLeuSerSergly 255
DB 126 CCGGGGAGCCCAACAGCGGGGCCAGGCGCAGAGACTGCGTGAATGACAGGCGCTCGGG 67
QY 236 ArgTrpAsnAspThRgLucyHsLeuThRMet---TyRPhenAlaCysGlu 271
DB 66 CAGTGAATGACGCGCTTCTGCGGAGCAGCTGCGTGAACGCGCTGGGTGTGAC 16

RESULT 11
US-09-535-521-10
; Sequence 10, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 417
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TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(417)
US-09-535-521-10

Alignment Scores:
Pred. No.: 9.79e-15 Length: 417
Score: 202.50 Matches: 44
Percent Similarity: 55.56% Conservative: 21
Best Local Similarity: 37.61% Mismatches: 47
Query Match: 13.65% Indels: 5
DB: GAPS: 3

US-09-600-932-2 (1-277) x US-09-535-521-10 (1-417)
QY 156 GUGLUYSPhETyTyrIleValGInGLuLulysAsnTyRArgLuseRLeuThRHis 175
DB 64 CAGAGGAAGTGCTACTACTGCGGAGAGAGCCCAAGAAGTGATCCAGCCCGTTGGCC 123
QY 176 CysArgIleArgGlyGlyMetLeuAlaMetProLysAspGluAlaIAsnThRleu 195
DB 124 TGCAGCAAGCTGCAAGGCGGCTGCCCATCCACAGCCAGAGGAGCAAGCACTTCTG 183
QY 196 AlaAspTyRValAlaLysSerGlyPhePheArgValPheIleGlyValAlaAsnThR 215
DB 184 GCCAGATATGCCAACAAGAGGC-----ACCTGATATGCGCTCCGGACCTGGAC 234
QY 216 ArgGluGlyGlnTyRMetPheThRAspAsnThRProLeuGlnAsnTyRserAsnThR 235
DB 235 AGAGAGGGGAGTTATCTGTGATGAGACGAGAACCCCTG---AACTATAGCAACTGCG 291
QY 236 GUGLUYluproSerAspProTyRgLyHsGluAspCysValGluMetLeuSerSergly 255
DB 292 CCGGGGAGCCCAACAGCGGGGCCAGGCGCAGAGACTGCGTGAATGACAGGCGCTCGGG 351
QY 256 ArgTrpAsnAspThRgLucyHsLeuThRMet---TyRPhenAlaCysGlu 271
DB 352 CAGTGAATGACGCGCTTCTGCGGAGCAGCTGCGTGAACGCGCTGGGTGTGAC 402
```

```
RESULT 12
US-09-535-521-12/C
; Sequence 12, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-12

Alignment Scores:
Pred. No.: 9.79e-15 Length: 417
Score: 202.50 Matches: 44
Percent Similarity: 55.56% Conservative: 21
Best Local Similarity: 37.61% Mismatches: 47
Query Match: 13.65% Indels: 5
DB: GAPS: 3

US-09-600-932-2 (1-277) x US-09-535-521-12 (1-417)
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QY 156 GUGLUGLUPHETRYTYRILEVALGUGLUGLUSANTYRARGLUSERLEUTHIS 175  
DB 354 CAGAGAGAGTGTCTACTCTGCGGAGAGGCCAAGAGTGCATCCAGCCGGTTGCC 295  
QY 176 CysArgIleArgGlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIle 195  
DB 294 TGCAGCAAGCTGCAGAGGCGCTGCGCATCCACAGCCAGAGGAGGAGACTTCTG 235  
QY 196 AlaAspTyrValAlaLysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlu 215  
DB 234 GCCAGGTATGCCAACAGAGGCG-----ACCTGATTTGGCCTCCGGAGACTTGCAG 184  
QY 216 ArgGluGluGlnTyrMetPheThrAspAsnThrProLeuGlnAsnTyrSerAspThrPsn 235  
DB 183 AGAGAGGGGAGAGTATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 127  
QY 236 GUGLUGLUPROSERASPRTOTRYGLYHISGLUASPCYVALGIMETLEUSERSERGLY 255  
DB 126 CCGGAG 67  
QY 256 ArgTyrAsnAspThrGluCysHisLeuThrMet---TyrPheValCysGlu 271  
DB 66 CAGTGAATGAG 16

## RESULT 13

US-09-535-521-13  
Sequence 13, Application US/09535521

Patent No. 6410714  
GENERAL INFORMATION:  
APPLICANT: Weber, Eric R.  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)  
FILE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
FILE REFERENCE: AL-5  
CURRENT APPLICATION NUMBER: US/09/535,521  
CURRENT FILING DATE: 2000-03-24  
EARLIER APPLICATION NUMBER: 60/125,913  
EARLIER FILING DATE: 1999-03-24  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 13  
LENGTH: 423  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(423)  
US-09-535-521-13

## Alignment Scores:

Pred. No.: 1e-14 Length: 423  
Score: 202.50 Matches: 44  
Percent Similarity: 55.56% Conservative: 21  
Best Local Similarity: 37.61% Mismatches: 47  
Query Match: 13.65% Indels: 5  
Gaps: 3

US-09-600-932-2 (1-277) x US-09-535-521-13 (1-423)

QY 156 GUGLUGLUPHETRYTYRILEVALGUGLUGLUSANTYRARGLUSERLEUTHIS 175  
DB 70 CAGAGAGAGTGTCTACTCTGCGGAGAGGCCAAGAGTGCATCCAGCCGGTTGCC 129  
QY 176 CysArgIleArgGlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIle 195  
DB 294 TGCAGCAAGCTGCAGAGGCGCTGCGCATCCACAGCCAGAGGAGGAGACTTCTG 189  
QY 196 AlaAspTyrValAlaLysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlu 215  
DB 234 GCCAGGTATGCCAACAGAGGCG-----ACCTGATTTGGCCTCCGGAGACTTGCAG 240  
QY 216 ArgGluGluGlnTyrMetPheThrAspAsnThrProLeuGlnAsnTyrSerAspThrPsn 235

DB 241 AGAGAGGAGAGTATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297  
QY 236 GUGLUGLUPROSERASPRTOTRYGLYHISGLUASPCYVALGIMETLEUSERSERGLY 255  
DB 298 CCGGAG 357  
QY 256 ArgTyrAsnAspThrGluCysHisLeuThrMet---TyrPheValCysGlu 271  
DB 358 CAGTGAATGAG 408

## RESULT 14

US-09-535-521-15/c  
Sequence 15, Application US/09535521

Patent No. 6410714  
GENERAL INFORMATION:  
APPLICANT: Weber, Eric R.  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)  
FILE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
FILE REFERENCE: AL-5  
CURRENT APPLICATION NUMBER: US/09/535,521  
CURRENT FILING DATE: 2000-03-24  
EARLIER APPLICATION NUMBER: 60/125,913  
EARLIER FILING DATE: 1999-03-24  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 15  
LENGTH: 423  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-535-521-15

## Alignment Scores:

Pred. No.: 1e-14 Length: 423  
Score: 202.50 Matches: 44  
Percent Similarity: 55.56% Conservative: 21  
Best Local Similarity: 37.61% Mismatches: 47  
Query Match: 13.65% Indels: 5  
Gaps: 3

US-09-600-932-2 (1-277) x US-09-535-521-15 (1-423)

QY 156 GUGLUGLUPHETRYTYRILEVALGUGLUGLUSANTYRARGLUSERLEUTHIS 175  
DB 354 CAGAGAGAGTGTCTACTCTGCGGAGAGGCCAAGAGTGCATCCAGCCGGTTGCC 295  
QY 176 CysArgIleArgGlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIle 195  
DB 294 TGCAGCAAGCTGCAGAGGCGCTGCGCATCCACAGCCAGAGGAGGAGACTTCTG 235  
QY 196 AlaAspTyrValAlaLysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlu 215  
DB 234 GCCAGGTATGCCAACAGAGGCG-----ACCTGATTTGGCCTCCGGAGACTTGCAG 184  
QY 216 ArgGluGluGlnTyrMetPheThrAspAsnThrProLeuGlnAsnTyrSerAspThrPsn 235  
DB 183 AGAGAGGAGAGTATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 127  
QY 236 GUGLUGLUPROSERASPRTOTRYGLYHISGLUASPCYVALGIMETLEUSERSERGLY 255  
DB 126 CCGGAG 67  
QY 256 ArgTyrAsnAspThrGluCysHisLeuThrMet---TyrPheValCysGlu 271  
DB 66 CAGTGAATGAG 16

## RESULT 15

US-09-535-521-16  
Sequence 16, Application US/09535521

Patent No. 6410714  
GENERAL INFORMATION:  
APPLICANT: Weber, Eric R.  
APPLICANT: McCall, Catherine A.

;; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)  
;; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
;; FILE REFERENCE: AL-5  
;; CURRENT APPLICATION NUMBER: US/09/535,521  
;; CURRENT FILING DATE: 2000-03-24  
;; EARLIER APPLICATION NUMBER: 60/125,913  
;; EARLIER FILING DATE: 1999-03-24  
;; NUMBER OF SEQ ID NOS: 26  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 16  
;; LENGTH: 561  
;; TYPE: DNA  
;; ORGANISM: Canis familiaris  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (1)..(561)  
US-09-535-521-16

## Alignment Scores:

Pred. No.:	1,52e-14	Length:	561
Score:	202.50	Matches:	44
Percent Similarity:	55.56%	Conservative:	21
Best Local Similarity:	37.61%	Mismatches:	47
Query Match:	13.65%	Indels:	5
DB:	4	Gaps:	3

US-09-600-932-2 (1-277) x US-09-535-521-16 (1-561)

```
QY 156 GIUGLULYSPhETTYRILEValGInGluLULysAsnTYRArgGluSerLeuThrHis 175
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 CAGAGAGAGTGTCTACTTCTGGCGAGAGGCCAAGAGTGTATCCAGCCCGGTTGCC 267
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 176 CysArgIleArgGlyGlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIle 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 268 TGCACCAAGCTGCAGAGGGCGCTGGCCAGATCCACAGCCCAAGAGAGCAGACTTCTG 327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 196 AlaAspTYRValAlaIleSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlu 215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 328 GCCAGGTATGCCAACAAGAGGC-----ACCTGATTTGGCTTCGGGACTGTGAC 378
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 216 ArgGluGlyGlnTYRMetPheThrAspAsnThrProLeuGluAsnTYRSerAsnTrpAsn 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 AGAGAGGGGGAGTTTATCTGTGATGAGCAGAACCCCTG---AACTATAGCAACTGGCGG 435
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 236 GIUGLYGluProSerAspProTYRGLYHisGluAspCysValGluMetLeuSerSerGly 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 CCGGGGAGACCCCAACACAGCGGGGCCAGGCGAGACTGTGTATGATGACAGGCGCTCGGG 495
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 256 ArgTrpAsnAspThrGluCysHisLeuThrMet---TYRpheValCysGlu 271
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 CAGTGTGATGAGCGCTTCTGGCGGACGTCGCTGTGAGCGCTGTGTGTGAC 546
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: June 15, 2003, 07:54:58  
Job time : 88 secs